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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:19 ; Search time 25.75 Seconds
(without alignments)
36.985 Million cell updates/sec

Title: US-09-881-490-150
Perfect score: 31
Sequence: 1 LIQLFH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query % | | | DB ID | Description |
|------------|---------|-------|--------|----------|--------------------|
| | Score | Match | Length | | |
| 1 | 31 | 100.0 | 6 | AAW04061 | Antifungal peptid |
| 2 | 31 | 100.0 | 6 | AAW44549 | Anti-fungal peptid |
| 3 | 31 | 100.0 | 6 | AAW00526 | Antifungal peptid |
| 4 | 31 | 100.0 | 6 | AAW65450 | Anti-fungal peptid |
| 5 | 31 | 100.0 | 7 | AAW04022 | Antifungal peptid |
| 6 | 31 | 100.0 | 7 | AAW04023 | Antifungal peptid |
| 7 | 31 | 100.0 | 7 | AAW44541 | Anti-fungal peptid |
| 8 | 31 | 100.0 | 7 | AAW44542 | Anti-fungal peptid |
| 9 | 31 | 100.0 | 7 | AAW43731 | Bactericidal/perme |

| | | | | | | |
|----|----|-------|---|----|----------|--------------------|
| 10 | 31 | 100.0 | 7 | 18 | AAW43732 | Bactericidal/perme |
| 11 | 31 | 100.0 | 7 | 20 | AAW00519 | Antifungal peptid |
| 12 | 31 | 100.0 | 7 | 20 | AAW00518 | Antifungal peptid |
| 13 | 31 | 100.0 | 7 | 22 | AAW65442 | Anti-fungal peptid |
| 14 | 31 | 100.0 | 7 | 22 | AAW65443 | Anti-fungal peptid |
| 15 | 31 | 100.0 | 8 | 17 | AAW04017 | Antifungal peptid |
| 16 | 31 | 100.0 | 8 | 17 | AAW04018 | Antifungal peptid |
| 17 | 31 | 100.0 | 8 | 17 | AAW04019 | Antifungal peptid |
| 18 | 31 | 100.0 | 8 | 18 | AAW44534 | Anti-fungal peptid |
| 19 | 31 | 100.0 | 8 | 18 | AAW44535 | Anti-fungal peptid |
| 20 | 31 | 100.0 | 8 | 18 | AAW44536 | Anti-fungal peptid |
| 21 | 31 | 100.0 | 8 | 18 | AAW43724 | Bactericidal/perme |
| 22 | 31 | 100.0 | 8 | 18 | AAW43725 | Bactericidal/perme |
| 23 | 31 | 100.0 | 8 | 18 | AAW43726 | Bactericidal/perme |
| 24 | 31 | 100.0 | 8 | 20 | AAW00511 | Antifungal peptid |
| 25 | 31 | 100.0 | 8 | 20 | AAW00512 | Antifungal peptid |
| 26 | 31 | 100.0 | 8 | 20 | AAW00513 | Antifungal peptid |
| 27 | 31 | 100.0 | 8 | 22 | AAW65435 | Anti-fungal peptid |
| 28 | 31 | 100.0 | 8 | 22 | AAW65436 | Anti-fungal peptid |
| 29 | 31 | 100.0 | 8 | 22 | AAW65437 | Anti-fungal peptid |
| 30 | 31 | 100.0 | 9 | 17 | AAW04011 | Antifungal peptid |
| 31 | 31 | 100.0 | 9 | 17 | AAW04012 | Antifungal peptid |
| 32 | 31 | 100.0 | 9 | 17 | AAW04013 | Antifungal peptid |
| 33 | 31 | 100.0 | 9 | 18 | AAW43720 | Bactericidal/perme |
| 34 | 31 | 100.0 | 9 | 18 | AAW43718 | Bactericidal/perme |
| 35 | 31 | 100.0 | 9 | 18 | AAW43719 | Bactericidal/perme |
| 36 | 31 | 100.0 | 9 | 18 | AAW44528 | Anti-fungal peptid |
| 37 | 31 | 100.0 | 9 | 18 | AAW44529 | Anti-fungal peptid |
| 38 | 31 | 100.0 | 9 | 18 | AAW44530 | Anti-fungal peptid |
| 39 | 31 | 100.0 | 9 | 20 | AAW00505 | Antifungal peptid |
| 40 | 31 | 100.0 | 9 | 20 | AAW00506 | Antifungal peptid |
| 41 | 31 | 100.0 | 9 | 20 | AAW00507 | Antifungal peptid |
| 42 | 31 | 100.0 | 9 | 22 | AAW68710 | Peptide-based cons |
| 43 | 31 | 100.0 | 9 | 22 | AAW65429 | Anti-fungal peptid |
| 44 | 31 | 100.0 | 9 | 22 | AAW65430 | Anti-fungal peptid |
| 45 | 31 | 100.0 | 9 | 22 | AAW65431 | Anti-fungal peptid |

ALIGNMENTS

RESULT 1

AAW04061

ID AAW04061 standard; peptide; 6 AA.

XX AAW04061;

AC AAW04061;

XX 04-NOV-1996 (first entry)

DT Antifungal peptide XMP.317.

XX

KW Antifungal peptide; inhibitor; Domain III; polymorphonuclear leukocyte;
KW bactericidal/permeability-increasing protein; BPI; mammalian; PMN; fungi;
KW neutrophil; replication inhibitor; fungal infection; Aspergillus;
KW Cryptococcus; Candida; C.albicans; C.galabrat; C.krusei; C.lusitaniae;
KW C.parapsilosis; C.tropicalis; therapy.

OS Synthetic.

XX

FH Key Location/Qualifiers
Ft Modified-site 6 /note= "amidated"

FT

XX WO9608509-A1.

PN

XX 21-MAR-1996.

PD

XX 20-JUL-1995; 95WO-US09262.

PF

XX 13-JAN-1995; 95US-0372105.

PR

PR 15-SEP-1994; 94US-0306473.

XX

PA (XOMA) XOMA CORP.

XX Fadem MB, Lim E, Little RG;
PI WPI: 1996-179900/18.
XX Antifungal peptide(s) derived from Domain III of BPI protein - used
PT in vitro for killing or inhibiting replication of fungi, esp.
PT Candida species
XX Claim 14; Page 150; 199pp; English.
PS
XX AAW04000-W04160 represent antifungal peptides. These sequences are
CC based on (or derived from) Domain III of the
CC bactericidal/permeability-increasing protein (BPI). BPI is a protein
CC that can be isolated from the granules of mammalian polymorphonuclear
CC leukocytes (PMNs or neutrophils). These antifungal peptides can be used
CC for killing, or inhibiting replication of, fungi in vitro. These
CC sequences can also be used for treatment of a fungal infection involving
CC fungi from the species Candida, Aspergillus and Cryptococcus. The
CC sequences are especially useful for treating C.albicans, C.galabrat,
CC C.krusei, C.lusitaniae, C.parapsilosis and C.tropicalis infections.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db : LIQLFH 6

RESULT 2
AAW44549
ID AAW44549 standard; peptide; 6 AA.
XX
AC AAW44549;
XX
DT 27-APR-1998 (first entry)
XX
DE Anti-fungal peptide #150 based on BPI protein (residues 142-169).
XX
KW Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.
XX
OS Synthetic.
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Modified-site 6 /note= "C-terminal amide"
FT
XX
XX WO9704008-A1.
PN
XX
PD 06-FEB-1997.
XX
XX 21-MAR-1996; 96WO-US03845.
PF
XX 20-JUL-1995; 95US-0504841.
PR
XX (XOMA) XOMA CORP.
PA
XX Fadem MB, Lim E, Little RG;
PI
XX WPI: 1997-132578/12.
DR
XX Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides
XX
PS Claim 1; Page 187; 230pp; English.
XX

CC This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db : LIQLFH 6

RESULT 3
AAY00526
ID AAY00526 standard; Peptide; 6 AA.
XX
AC AAY00526;
XX
DT 07-MAY-1999 (first entry)
XX
DE Antifungal peptide XMP.317.
XX
KW Antifungal; BPI; bactericidal/permeability increasing protein;
KW Candida infection.
XX
OS Synthetic.
XX
PN US5858974-A.
XX
PD 12-JAN-1999.
XX
PF 21-MAR-1996; 96US-0621259.
XX
PR 21-MAR-1996; 96US-0621259.
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;
XX
DR WPI: 1999-119956/10.
XX
PT Antifungal peptides - comprising part of bactericidal or
PT permeability-increasing protein sequence or related sequence
XX
PS Disclosure; Columns 157-158; 132pp; English.
XX
CC New peptides are provided which are based on Domain III (amino acids
CC 142-169) of human bactericidal/permeability-increasing protein (BPI).
CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGWLIQLFHKR) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, IQLF, WLIQL, LIQLF and WLIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (Ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of
CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitaniae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIQLFH 6
IIIII
DB 1 LIQLFH 6

RESULT 4
AAB65450
ID AAB65450 standard; Peptide: 6 AA.
XX
AC AAB65450;
XX
XX
DT 27-MAR-2001 (first entry)
XX
DE Anti-fungal peptide XMP.317.
XX
KW Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;
KW bactericidal/permeability-increasing protein; bactericidal;
KW fungal infection.
XX Homo sapiens.
XX
XX US6156730-A.
PN
XX
PD 05-DEC-2000.
XX
XX 08-JAN-1999; 99US-0227659.
PF
XX 21-MAR-1996; 96US-0621259.
PR 12-MAR-1993; 93US-0030644.
PR 15-JUL-1993; 93US-0093202.
PR 14-JAN-1994; 94US-0183222.
PR 11-MAR-1994; 94US-0209762.
PR 11-JUL-1994; 94US-0273540.
PR 15-SEP-1994; 94US-0306473.
PR 13-JAN-1995; 95US-0372105.
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
XX Lim E, Fadem MB, Little RG;
PI
XX WPI; 2001-090160/10.
DR
XX Novel anti-fungal peptides derived from domain III of
PT bactericidal/permeability-increasing protein useful for killing or
PT inhibiting replication of fungi and for treating fungal infections -
XX
XX Example 2; Columns 163-164; 134pp; English.
PS
XX The present invention relates to antifungal peptides (see
CC AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C.albicans, C.glabrata, C.krusei,
CC C.lusitaniae, C.parapsilosis and C.tropicalis.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIQLFH 6
IIIII

Db 1 LIQLFH 6

RESULT 5
AAW04022
ID AAW04022 standard; peptide: 7 AA.
XX
AC AAW04022;
XX
XX 31-OCT-1996 (first entry)
XX
DE Antifungal peptide XMP.309.
XX
KW Antifungal peptide; inhibitor; Domain III; polymorphonuclear leukocyte;
KW bactericidal/permeability-increasing protein; BPI; mammalian; PMN; fungl;
KW neutrophil; replication inhibitor; fungal infection; Aspergillus;
KW Cryptococcus; Candida; C.albicans; C.glabrat; C.krusei; C.lusitaniae;
KW C.parapsilosis; C.tropicalis; therapy.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 7 /note= "amidated"
FT
XX W09608509-A1.
PN
XX 21-MAR-1996.
PD
XX 20-JUL-1995; 95WO-US09262.
PF
XX 13-JAN-1995; 95US-0372105.
PR 15-SEP-1994; 94US-0306473.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;
XX WPI; 1996-179900/18.
DR
XX Antifungal peptide(s) derived from Domain III of BPI protein - used
PT in vitro for killing or inhibiting replication of fungi, esp.
PT Candida species
XX
PS Claim 5; Page 147; 199pp; English.
XX
CC AAW04000-W04160 represent antifungal peptides. These sequences are
CC based on (or derived from) Domain III of the
CC bactericidal/permeability-increasing protein (BPI). BPI is a protein
CC that can be isolated from the granules of mammalian polymorphonuclear
CC leukocytes (PMNs or neutrophils). These antifungal peptides can be used
CC for killing, or inhibiting replication of, fungi in vitro. These
CC sequences can also be used for treatment of a fungal infection involving
CC fungi from the species Candida, Aspergillus and Cryptococcus. The
CC sequences are especially useful for treating C.albicans, C.glabrat,
CC C.krusei, C.lusitaniae, C.parapsilosis and C.tropicalis infections.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIQLFH 6
IIIII
DB 2 LIQLFH 7

RESULT 6
AAW04023
ID AAW04023 standard; peptide: 7 AA.
XX
AC AAW04023;

```
XX 31-OCT-1996 (first entry)
DT
XX Antifungal peptide XMP.310.
DE
XX Antifungal peptide; inhibitor; Domain III; polymorphonuclear leukocyte;
KW bactericidal/permeability-increasing protein; BPI; mammalian; PMN; fungi;
KW neutrophil; replication inhibitor; fungal infection; Aspergillus;
KW Cryptococcus; Candida; C.albicans; C.galabrati; C.krusei; C.lusitaniae;
KW C.parapsilosis; C.tropicalis; therapy.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 7 /note= "amidated"
FT
XX WO9608509-A1.
PN
XX 21-MAR-1996.
PD
XX
XX 20-JUL-1995; 95WO-US09262.
PF
XX 13-JAN-1995; 95US-0372105.
XX
PR 15-SEP-1994; 94US-0306473.
PR
XX (XOMA ) XOMA CORP.
PA
XX Fadem MB, Lim E, Little RG;
XX WPI; 1996-179900/18.
XX
XX Antifungal peptide(s) derived from Domain III of BPI protein - used
PT in vitro for killing or inhibiting replication of fungi, esp.
PT Candida species
PT
XX
PS Claim 5; Page 147; 199pp; English.
PS
XX AAW04000-W04160 represent antifungal peptides. These sequences are
CC based on (or derived from) Domain III of the
CC bactericidal/permeability-increasing protein (BPI). BPI is a protein
CC that can be isolated from the granules of mammalian polymorphonuclear
CC leukocytes (PMNs or neutrophils). These antifungal peptides can be used
CC for killing, or inhibiting replication of, fungi in vitro. These
CC sequences can also be used for treatment of a fungal infection involving
CC fungi from the species Candida, Aspergillus and Cryptococcus. The
CC sequences are especially useful for treating C.albicans, C.galabrati,
CC C.krusei, C.lusitaniae, C.parapsilosis and C.tropicalis infections.
XX
SQ Sequence 7 AA;
XX
XX Query Match 100.0%; Score 31; DB 17; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 LIQLFH 6
DB 1 LIQLFH 6
XX
RESULT 7
AAW44541
ID AAW44541 standard; peptide; 7 AA.
XX
AC AAW44541;
XX
XX 27-APR-1998 (first entry)
DT
XX Anti-fungal peptide #142 based on BPI protein (residues 142-169).
DE
XX Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.
KW
XX
```

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OS Synthetic.
OS Mammalia.
XX
XX Key Location/Qualifiers
FT Modified-site 7 /note= "C-terminal amide"
FT
XX WO9704008-A1.
PN
XX 06-FEB-1997.
XX
XX 21-MAR-1996; 96WO-US03845.
PF
XX 20-JUL-1995; 95US-0504841.
XX
XX (XOMA ) XOMA CORP.
PA
XX Fadem MB, Lim E, Little RG;
XX WPI; 1997-132578/12.
XX
XX Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides
PT
XX Claim 1; Page 184; 230pp; English.
PS
XX This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.
XX
SQ Sequence 7 AA;
XX
XX Query Match 100.0%; Score 31; DB 18; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 LIQLFH 6
DB 2 LIQLFH 7
XX
RESULT 8
AAW44542
ID AAW44542 standard; peptide; 7 AA.
XX
XX AAW44542;
XX
XX 27-APR-1998 (first entry)
DT
XX Anti-fungal peptide #143 based on BPI protein (residues 142-169).
DE
XX Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.
KW
XX Synthetic.
XX OS Mammalia.
XX
XX Key Location/Qualifiers
FT Modified-site 7 /note= "C-terminal amide"
FT
XX WO9704008-A1.
PN
XX 06-FEB-1997.
XX
XX 21-MAR-1996; 96WO-US03845.
PF
XX 20-JUL-1995; 95US-0504841.
XX
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XX (XOMA) XOMA CORP.
XX Fadem MB, Lim E, Little RG;
XX WPI; 1997-132578/12.
XX Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal/permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides
XX Claim 1; Page 184; 230pp; English.
XX This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 31; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LIQLFH 6
Db 1 LIQLFH 6
RESULT 9
AAW43731
ID AAW43731 standard; peptide; 7 AA.
XX
AC AAW43731;
XX
DT 20-APR-1998 (first entry)
XX
DE Bactericidal/permeability increasing peptide XMP.309.
XX
KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW bacterial infection; fungal infection; endotoxin; heparin;
KW angiogenesis; fungicidal; recombinant DNA; vector.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 7 /note= "Amidated"
FT
XX
PN WO9735009-A1.
XX
PD 25-SEP-1997.
XX
PF 18-MAR-1997; 97WO-US05287.
XX
PR 22-MAR-1996; 96US-0621803.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD;
XX
DR WPI; 1997-480215/44.
XX
PT Recombinant production of bactericidal/permeability increasing
PT protein - by expression as a fusion protein in microbial host cells,
PT then cleaving the BPI peptide from the carrier
XX
PS Claim 10; Page 119; 186pp; English.

CC A new recombinant DNA vector construct has been developed which encodes
CC a fusion protein and is suitable for introduction into a bacterial host.
CC The vector comprises: (a) DNA encoding at least one cationic
CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC located between (a) and (b). The present sequence represents a
CC specifically claimed BPI peptide. The peptide sequence represents a
CC the treatment of bacterial and fungal infections. BPI peptides also
CC bind to endotoxins and heparin, neutralising their effects. The
CC peptides have further been shown to inhibit angiogenesis (partly due to
CC heparin-binding activity). The fusion proteins have been found to be
CC expressed in large amounts without significant proteolysis, and in some
CC cases are actually secreted from the host cells. This allows the
CC indirect production of anti-microbial BPI peptides in microbial hosts.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 31; DB 18; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LIQLFH 6
Db 2 LIQLFH 7
RESULT 10
AAW43732
ID AAW43732 standard; peptide; 7 AA.
XX
AC AAW43732;
XX
DT 20-APR-1998 (first entry)
XX
DE Bactericidal/permeability increasing peptide XMP.310.
XX
KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW bacterial infection; fungal infection; endotoxin; heparin;
KW angiogenesis; fungicidal; recombinant DNA; vector.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 7 /note= "Amidated"
FT
XX
PN WO9735009-A1.
XX
PD 25-SEP-1997.
XX
PF 18-MAR-1997; 97WO-US05287.
XX
PR 22-MAR-1996; 96US-0621803.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD;
XX
DR WPI; 1997-480215/44.
XX
PT Recombinant production of bactericidal/permeability increasing
PT protein - by expression as a fusion protein in microbial host cells,
PT then cleaving the BPI peptide from the carrier
XX
PS Claim 10; Page 119; 186pp; English.
XX
CC A new recombinant DNA vector construct has been developed which encodes
CC a fusion protein and is suitable for introduction into a bacterial host.
CC The vector comprises: (a) DNA encoding at least one cationic
CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC located between (a) and (b). The present sequence represents a
CC specifically claimed BPI peptide. The peptide sequence represents a
CC the treatment of bacterial and fungal infections. BPI peptides also
CC bind to endotoxins and heparin, neutralising their effects. The
CC peptides have further been shown to inhibit angiogenesis (partly due to
CC heparin-binding activity). The fusion proteins have been found to be
CC expressed in large amounts without significant proteolysis, and in some
CC cases are actually secreted from the host cells. This allows the
CC indirect production of anti-microbial BPI peptides in microbial hosts.
XX
SQ Sequence 7 AA;

CC specifically claimed BPI peptide. The peptides have many uses including
CC the treatment of bacterial and fungal infections. BPI peptides also
CC bind to endotoxins and heparin, neutralising their effects. The
CC peptides have further been shown to inhibit angiogenesis (partly due to
CC heparin-binding activity). The fusion proteins have been found to be
CC expressed in large amounts without significant proteolysis, and in some
CC cases are actually secreted from the host cells. This allows the
CC indirect production of anti-microbial BPI peptides in microbial hosts.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 18; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
| | | | |
Db 1 LIQLFH 6

RESULT 11
AAAY00519
ID AAAY00519 standard; Peptide; 7 AA.

XX AC AAAY00519;
XX DT 07-MAY-1999 (first entry)
XX DE Antifungal peptide XMP.310.

XX KW Antifungal; BPI; bactericidal/permeability increasing protein;
KW KW Candida infection.

XX OS Synthetic.
XX PN US5858974-A.
XX PD 12-JAN-1999.

XX PF 21-MAR-1996; 96US-0621259.
XX PR 21-MAR-1996; 96US-0621259.
XX PR 20-JUL-1995; 95US-0504841.

XX PA (XOMA) XOMA CORP.

XX PI Fadem MB, Lim E, Little RG;

XX PX WPI; 1999-119956/10.

XX DR Antifungal peptides - comprising part of bactericidal or
PT permeability-increasing protein sequence or related sequence

XX PS Disclosure; Columns 153-154; 132pp; English.

XX CC New peptides are provided which are based on Domain III (amino acids
CC 142-169) of human bactericidal/permeability-increasing protein (BPI).
CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGWLIQLFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, IQLF, WLIQL, LIQLF and WLIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of
CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
| | | | |
Db 1 LIQLFH 6

RESULT 12
AAAY00518
ID AAAY00518 standard; Peptide; 7 AA.

XX AC AAAY00518;
XX DT 07-MAY-1999 (first entry)
XX DE Antifungal peptide XMP.309.

XX KW Antifungal; BPI; bactericidal/permeability increasing protein;
KW KW Candida infection.

XX OS Synthetic.
XX PN US5858974-A.
XX PD 12-JAN-1999.

XX PF 21-MAR-1996; 96US-0621259.
XX PR 21-MAR-1996; 96US-0621259.
XX PR 20-JUL-1995; 95US-0504841.

XX PA (XOMA) XOMA CORP.

XX PI Fadem MB, Lim E, Little RG;

XX PX WPI; 1999-119956/10.

XX PT Antifungal peptides - comprising part of bactericidal or
PT permeability-increasing protein sequence or related sequence

XX PS Disclosure; Columns 153-154; 132pp; English.

XX CC New peptides are provided which are based on Domain III (amino acids
CC 142-169) of human bactericidal/permeability-increasing protein (BPI).
CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGWLIQLFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, IQLF, WLIQL, LIQLF and WLIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of
CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
| | | | |
Db 2 LIQLFH 7

RESULT 13
AAB65442
ID AAB65442 standard; Peptide; 7 AA.

XX AC AAB65442;
DT 27-MAR-2001 (first entry)
XX DE Anti-fungal peptide XMP.309.
XX KW Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;
KW bactericidal/permeability-increasing protein; bactericidal;
KW fungal infection.

XX OS Homo sapiens.
XX PN US6156730-A.
XX PD 05-DEC-2000.
XX PF 08-JAN-1999; 99US-0227659.
XX PR 21-MAR-1996; 96US-0621259.
PR 12-MAR-1993; 93US-0030644.
PR 15-JUL-1993; 93US-0093202.
PR 14-JAN-1994; 94US-0183222.
PR 11-MAR-1994; 94US-0209762.
PR 11-JUL-1994; 94US-0273540.
PR 15-SEP-1994; 94US-0306473.
PR 13-JAN-1995; 95US-0372105.
PR 20-JUL-1995; 95US-0504841.

XX (XOMA) XOMA CORP.
XX PI Lim E, Fadem MB, Little RG;
XX WPI; 2001-090160/10.

XX Novel anti-fungal peptides derived from domain III of
PT bactericidal/permeability-increasing protein useful for killing or
PT inhibiting replication of fungi and for treating fungal infections -
XX Example 2; Columns 157-158; 134pp; English.

XX The present invention relates to antifungal peptides (see
CC AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C.albicans, C.glabrata, C.krusei,
CC C.lusitaniae, C.parapsilosis and C.tropicalis.

XX SQ Sequence 7 AA;
Query Match 100.0%; Score 31; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
DB 2 LIQLFH 7

RESULT 14
AAB65443
ID AAB65443 standard; Peptide; 7 AA.
XX AC AAB65443;
XX

DT 27-MAR-2001 (first entry)
XX DE Anti-fungal peptide XMP.310.

XX KW Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;
KW bactericidal/permeability-increasing protein; bactericidal;
KW fungal infection.
XX OS Homo sapiens.
XX PN US6156730-A.
XX PD 05-DEC-2000.
XX PF 08-JAN-1999; 99US-0227659.
XX PR 21-MAR-1996; 96US-0621259.
PR 12-MAR-1993; 93US-0030644.
PR 15-JUL-1993; 93US-0093202.
PR 14-JAN-1994; 94US-0183222.
PR 11-MAR-1994; 94US-0209762.
PR 11-JUL-1994; 94US-0273540.
PR 15-SEP-1994; 94US-0306473.
PR 13-JAN-1995; 95US-0372105.
PR 20-JUL-1995; 95US-0504841.

XX (XOMA) XOMA CORP.
XX PI Lim E, Fadem MB, Little RG;
XX WPI; 2001-090160/10.

XX Novel anti-fungal peptides derived from domain III of
PT bactericidal/permeability-increasing protein useful for killing or
PT inhibiting replication of fungi and for treating fungal infections -
XX Example 2; Columns 157-158; 134pp; English.

XX The present invention relates to antifungal peptides (see
CC AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C.albicans, C.glabrata, C.krusei,
CC C.lusitaniae, C.parapsilosis and C.tropicalis.

XX SQ Sequence 7 AA;
Query Match 100.0%; Score 31; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
DB 1 LIQLFH 6

RESULT 15
AAW04017
ID AAW04017 standard; peptide; 8 AA.
XX AC AAW04017;
XX DT 31-OCT-1996 (first entry)
XX DE Antifungal peptide XMP.302.
XX KW Antifungal peptide; inhibitor; Domain III; polymorphonuclear leukocyte;
KW bactericidal/permeability-increasing protein; BPI; mammalian; PMN; fungi;

KW neutrophil; replication inhibitor; fungal infection; Aspergillus;
KW Cryptococcus; Candida; C.albicans; C.galabrat; C.krusei; C.lusitaniae;
KW C.parapsilosis; C.tropicalis; therapy.

OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 8
FT /note= "amidated"

XX
PN WO9608509-A1.

XX
PD 21-MAR-1996.

XX
PF 20-JUL-1995; 95WO-US09262.

XX
PR 13-JAN-1995; 95US-0372105.

XX
PR 15-SEP-1994; 94US-0306473.

XX
PA (XOMA) XOMA CORP.

XX
PI Fadem MB, Lim E, Little RG;

XX
DR WPI; 1996-179900/18.

XX
PT Antifungal peptide(s) derived from Domain III of BPI protein - used
PT in vitro for killing or inhibiting replication of fungi, esp.
PT Candida species

XX
PS Claim 5; Page 144; 199pp; English.

XX
CC AAW04000-W04160 represent antifungal peptides. These sequences are
CC based on (or derived from) Domain III of the
CC bactericidal/permeability-increasing protein (BPI). BPI is a protein
CC that can be isolated from the granules of mammalian polymorphonuclear
CC leukocytes (PMNs or neutrophils). These antifungal peptides can be used
CC for killing, or inhibiting replication of, fungi in vitro. These
CC sequences can also be used for treatment of a fungal infection involving
CC fungi from the species Candida, Aspergillus and Cryptococcus. The
CC sequences are especially useful for treating C.albicans, C.galabrat,
CC C.krusei, C.lusitaniae, C.parapsilosis and C.tropicalis infections.

XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 31; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6

Db 3 LIQLFH 8

Search completed: October 14, 2003, 14:41:30
Job time : 25.9167 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:23 ; Search time 8.5 Seconds
(without alignments)
29.866 Million cell updates/sec

Title: US-09-881-490-150
Perfect score: 31
Sequence: 1 LIQLFH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| Result No. | Score | Query Match % | Length | DB ID | Description |
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| 2 | 31 | 100.0 | 6 | 5 | PCT-US95-09262-150 |
| 3 | 31 | 100.0 | 7 | 2 | US-08-621-803-175 |
| 4 | 31 | 100.0 | 7 | 2 | US-08-621-803-176 |
| 5 | 31 | 100.0 | 7 | 2 | US-08-621-259A-142 |
| 6 | 31 | 100.0 | 7 | 2 | US-08-621-259A-143 |
| 7 | 31 | 100.0 | 7 | 3 | US-09-217-352-175 |
| 8 | 31 | 100.0 | 7 | 3 | US-09-217-352-176 |
| 9 | 31 | 100.0 | 7 | 5 | PCT-US95-09262-142 |
| 10 | 31 | 100.0 | 7 | 5 | PCT-US95-09262-143 |
| 11 | 31 | 100.0 | 8 | 2 | US-08-621-803-168 |
| 12 | 31 | 100.0 | 8 | 2 | US-08-621-803-169 |
| 13 | 31 | 100.0 | 8 | 2 | US-08-621-803-170 |
| 14 | 31 | 100.0 | 8 | 2 | US-08-621-259A-135 |
| 15 | 31 | 100.0 | 8 | 2 | US-08-621-259A-136 |
| 16 | 31 | 100.0 | 8 | 2 | US-08-621-259A-137 |
| 17 | 31 | 100.0 | 8 | 3 | US-09-217-352-168 |
| 18 | 31 | 100.0 | 8 | 3 | US-09-217-352-169 |
| 19 | 31 | 100.0 | 8 | 3 | US-09-217-352-170 |
| 20 | 31 | 100.0 | 8 | 5 | PCT-US95-09262-135 |
| 21 | 31 | 100.0 | 8 | 5 | PCT-US95-09262-136 |
| 22 | 31 | 100.0 | 8 | 5 | PCT-US95-09262-137 |
| 23 | 31 | 100.0 | 9 | 2 | US-08-621-803-162 |
| 24 | 31 | 100.0 | 9 | 2 | US-08-621-803-163 |
| 25 | 31 | 100.0 | 9 | 2 | US-08-621-803-164 |
| 26 | 31 | 100.0 | 9 | 2 | US-08-621-259A-129 |
| 27 | 31 | 100.0 | 9 | 2 | US-08-621-259A-130 |

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| 28 | 31 | 100.0 | 9 | 2 | US-08-621-259A-131 | Sequence 131, App |
| 29 | 31 | 100.0 | 9 | 3 | US-09-217-352-162 | Sequence 162, App |
| 30 | 31 | 100.0 | 9 | 3 | US-09-217-352-163 | Sequence 163, App |
| 31 | 31 | 100.0 | 9 | 3 | US-09-217-352-164 | Sequence 164, App |
| 32 | 31 | 100.0 | 9 | 4 | US-09-344-541A-10 | Sequence 10, Appl |
| 33 | 31 | 100.0 | 9 | 5 | PCT-US95-09262-129 | Sequence 129, App |
| 34 | 31 | 100.0 | 9 | 5 | PCT-US95-09262-130 | Sequence 130, App |
| 35 | 31 | 100.0 | 9 | 5 | PCT-US95-09262-131 | Sequence 131, App |
| 36 | 31 | 100.0 | 10 | 2 | US-08-621-803-157 | Sequence 157, App |
| 37 | 31 | 100.0 | 10 | 2 | US-08-621-803-158 | Sequence 158, App |
| 38 | 31 | 100.0 | 10 | 2 | US-08-621-803-159 | Sequence 159, App |
| 39 | 31 | 100.0 | 10 | 2 | US-08-621-803-209 | Sequence 209, App |
| 40 | 31 | 100.0 | 10 | 2 | US-08-621-803-210 | Sequence 210, App |
| 41 | 31 | 100.0 | 10 | 2 | US-08-621-803-211 | Sequence 211, App |
| 42 | 31 | 100.0 | 10 | 2 | US-08-621-803-212 | Sequence 212, App |
| 43 | 31 | 100.0 | 10 | 2 | US-08-621-803-213 | Sequence 213, App |
| 44 | 31 | 100.0 | 10 | 2 | US-08-621-803-214 | Sequence 214, App |
| 45 | 31 | 100.0 | 10 | 2 | US-08-621-803-215 | Sequence 215, App |

ALIGNMENTS

RESULT 1

US-08-621-259A-150

; Sequence 150, Application US/08621259A

; Patent No. 5858974

; GENERAL INFORMATION:

; APPLICANT: Little II, Roger G

; APPLICANT: Lim, Edward

; APPLICANT: Fadem, Mitchell B.

; TITLE OF INVENTION: Anti-Fungal Peptides

; NUMBER OF SEQUENCES: 252

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McAndrews, Held & Malloy, Ltd.

; STREET: 500 West Madison Street

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60661

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/621,259A

; FILING DATE: 21-MAR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/504,841

; FILING DATE: 20-JUL-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: McNicholas, Janet M.

; REGISTRATION NUMBER: 32,918

; REFERENCE/DOCKET NUMBER: 11021US02

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/707-8889

; TELEFAX: 312/707-9155

; TELEX:

; INFORMATION FOR SEQ ID NO: 150:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: misc.feature

; OTHER INFORMATION: "XMP.317"

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: C-Terminus

; OTHER INFORMATION: /label= Amidation

; OTHER INFORMATION: /note= "The C-Terminus is Amidated."

US-08-621-259A-150

Query Match 100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 1 LIQLFH 6

RESULT 2

PCT-US95-09262-150
Sequence 150, Application PC/TUS9509262

GENERAL INFORMATION:

APPLICANT: Anti-Fungal Peptides

TITLE OF INVENTION: 205

NUMBER OF SEQUENCES: 205

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/09262

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/372,105

FILING DATE: 13-JAN-95

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/306,473

FILING DATE: 15-SEP-94

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/273,540

FILING DATE: 11-JUL-94

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/209,762

FILING DATE: 11-MAR-94

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/183,222

FILING DATE: 14-JAN-94

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/093,202

FILING DATE: 15-JUL-93

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/030,644

FILING DATE: 12-MAR-93

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.

REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27129/10040

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 150:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: "XMP.317"

FEATURE:

NAME/KEY: Modified-site

LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-150

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 1 LIQLFH 6

RESULT 3

US-08-621-803-175

Sequence 175, Application US/08621803

Patent No. 5851802

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

TITLE OF INVENTION: Methods for Recombinant Microbial Production of

TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/621,803

FILING DATE: 22-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.

REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27129/33199

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 175:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: "XMP.309"

FEATURE:

NAME/KEY: Modified-site

LOCATION: C-Terminus

OTHER INFORMATION: /label= Amidation

OTHER INFORMATION: /note= "The C-Terminus is Amidated."

US-08-621-803-175

Query Match

100.0%; Score 31; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 2 LIQLFH 7

RESULT 4

US-08-621-803-176

```
; Sequence 176, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; FUSION PROTEINS AND BPI-DERIVED PEPTIDES
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 176:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.310"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
; US-08-621-803-176

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 1 LIQLFH 6

RESULT 5
US-08-621-259A-142
; Sequence 142, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.309"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
; US-08-621-259A-142

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 2 LIQLFH 7

RESULT 6
US-08-621-259A-143
; Sequence 143, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
```

REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11021US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX:
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.310"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated."

US-08-621-259A-143

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
|||||
DB 1 LIQLFH 6

RESULT 7

US-09-217-352-175
Sequence 175, Application US/09217352
Patent No. 6274344
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217.352
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 175:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.309"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated."

US-09-217-352-175

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
|||||
DB 2 LIQLFH 7

RESULT 8

US-09-217-352-176
Sequence 176, Application US/09217352
Patent No. 6274344
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,352
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 176:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.310"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated."

US-09-217-352-176

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
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Db 1 LIQLFH 6

RESULT 9
PCT-US95-09262-142
; Sequence 142, Application PC/TUS9509262
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09262
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 15-JUL-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/10040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.309"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated"

PCT-US95-09262-142

Query Match 100.0%; Score 31; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. NO. 2.5e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
| | | | |
Db 2 LIQLFH 7

RESULT 10
PCT-US95-09262-143
; Sequence 143, Application PC/TUS9509262
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09262
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/10040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.310"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated"

PCT-US95-09262-143

Query Match 100.0%; Score 31; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
|||||
Db 1 LIQLFH 6

RESULT 11

US-08-621-803-168
; Sequence 168, Application US/08621803
; Patent No. 5851802

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides

; NUMBER OF SEQUENCES: 265

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/621,803

; FILING DATE: 22-MAR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Borun, Michael F.

; REGISTRATION NUMBER: 25,447

; REFERENCE/DOCKET NUMBER: 27129/33199

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 168:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; FEATURE:

; MOLECULE TYPE: peptide

; NAME/KEY: misc.feature

; OTHER INFORMATION: "XMP.302"

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: C-Terminus

; OTHER INFORMATION: /label= Amidation

; OTHER INFORMATION: /note= "The C-Terminus is Amidated."

US-08-621-803-168

Query Match 100.0%; Score 31; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
|||||
Db 3 LIQLFH 8

RESULT 12

US-08-621-803-169

; Sequence 169, Application US/08621803

; Patent No. 5851802

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides

; NUMBER OF SEQUENCES: 265

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/621,803

; FILING DATE: 22-MAR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Borun, Michael F.

; REGISTRATION NUMBER: 25,447

; REFERENCE/DOCKET NUMBER: 27129/33199

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 169:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: misc.feature

; OTHER INFORMATION: "XMP.303"

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: C-Terminus

; OTHER INFORMATION: /label= Amidation

; OTHER INFORMATION: /note= "The C-Terminus is Amidated."

US-08-621-803-169

Query Match 100.0%; Score 31; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
|||||
Db 2 LIQLFH 7

RESULT 13

US-08-621-803-170

; Sequence 170, Application US/08621803

; Patent No. 5851802

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; TITLE OF INVENTION: Methods for Recombinant Microbial Production of

; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides

; NUMBER OF SEQUENCES: 265

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25


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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.304"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-803-170
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Query Match 100.0%; Score 31; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LIQLFH 6
Db 1 LIQLFH 6
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RESULT 14
US-08-621-259A-135
; Sequence 135, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 135:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.302"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-135

Query Match 100.0%; Score 31; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIQLFH 6
Db 3 LIQLFH 8

RESULT 15
US-08-621-259A-136
; Sequence 136, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.303"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
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OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-136

Query Match 100.0%; Score 31; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIQLFH 6
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Db 2 LIQLFH 7

Search completed: October 14, 2003, 14:42:45
Job time : 9.5 secs

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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:34:14 ; Search time 14.625 Seconds
(without alignments)
66.104 Million cell updates/sec

Title: US-09-881-490-150
Perfect score: 31
Sequence: 1 LIQLFH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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- 10: /cgn2_5/ptodata/2/pubpaa/US09R_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------------------------|
| 1 | 31 | 100.0 | 6 | 9 | US-09-881-490-150 Sequence 150, App |
| 2 | 31 | 100.0 | 7 | 9 | US-09-765-527-175 Sequence 175, App |
| 3 | 31 | 100.0 | 7 | 9 | US-09-765-527-176 Sequence 176, App |
| 4 | 31 | 100.0 | 7 | 9 | US-09-881-490-142 Sequence 142, App |
| 5 | 31 | 100.0 | 7 | 9 | US-09-881-490-143 Sequence 143, App |
| 6 | 31 | 100.0 | 8 | 9 | US-09-765-527-168 Sequence 168, App |
| 7 | 31 | 100.0 | 8 | 9 | US-09-765-527-169 Sequence 169, App |
| 8 | 31 | 100.0 | 8 | 9 | US-09-765-527-170 Sequence 170, App |
| 9 | 31 | 100.0 | 8 | 9 | US-09-881-490-135 Sequence 135, App |
| 10 | 31 | 100.0 | 8 | 9 | US-09-881-490-136 Sequence 136, App |
| 11 | 31 | 100.0 | 8 | 9 | US-09-881-490-137 Sequence 137, App |
| 12 | 31 | 100.0 | 9 | 9 | US-09-765-527-162 Sequence 162, App |
| 13 | 31 | 100.0 | 9 | 9 | US-09-765-527-163 Sequence 163, App |
| 14 | 31 | 100.0 | 9 | 9 | US-09-765-527-164 Sequence 164, App |
| 15 | 31 | 100.0 | 9 | 9 | US-09-881-490-129 Sequence 129, App |

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| 16 | 31 | 100.0 | 9 | 9 | US-09-881-490-130 Sequence 130, App |
| 17 | 31 | 100.0 | 9 | 9 | US-09-881-490-131 Sequence 131, App |
| 18 | 31 | 100.0 | 10 | 9 | US-09-765-527-157 Sequence 157, App |
| 19 | 31 | 100.0 | 10 | 9 | US-09-765-527-158 Sequence 158, App |
| 20 | 31 | 100.0 | 10 | 9 | US-09-765-527-159 Sequence 159, App |
| 21 | 31 | 100.0 | 10 | 9 | US-09-765-527-209 Sequence 209, App |
| 22 | 31 | 100.0 | 10 | 9 | US-09-765-527-210 Sequence 210, App |
| 23 | 31 | 100.0 | 10 | 9 | US-09-765-527-211 Sequence 211, App |
| 24 | 31 | 100.0 | 10 | 9 | US-09-765-527-212 Sequence 212, App |
| 25 | 31 | 100.0 | 10 | 9 | US-09-765-527-213 Sequence 213, App |
| 26 | 31 | 100.0 | 10 | 9 | US-09-765-527-214 Sequence 214, App |
| 27 | 31 | 100.0 | 10 | 9 | US-09-765-527-215 Sequence 215, App |
| 28 | 31 | 100.0 | 10 | 9 | US-09-765-527-227 Sequence 227, App |
| 29 | 31 | 100.0 | 10 | 9 | US-09-881-490-124 Sequence 124, App |
| 30 | 31 | 100.0 | 10 | 9 | US-09-881-490-125 Sequence 125, App |
| 31 | 31 | 100.0 | 10 | 9 | US-09-881-490-126 Sequence 126, App |
| 32 | 31 | 100.0 | 10 | 9 | US-09-881-490-184 Sequence 184, App |
| 33 | 31 | 100.0 | 10 | 9 | US-09-881-490-185 Sequence 185, App |
| 34 | 31 | 100.0 | 10 | 9 | US-09-881-490-186 Sequence 186, App |
| 35 | 31 | 100.0 | 10 | 9 | US-09-881-490-187 Sequence 187, App |
| 36 | 31 | 100.0 | 10 | 9 | US-09-881-490-188 Sequence 188, App |
| 37 | 31 | 100.0 | 10 | 9 | US-09-881-490-190 Sequence 190, App |
| 38 | 31 | 100.0 | 10 | 9 | US-09-881-490-194 Sequence 194, App |
| 39 | 31 | 100.0 | 10 | 9 | US-09-881-490-195 Sequence 195, App |
| 40 | 31 | 100.0 | 10 | 9 | US-09-881-490-196 Sequence 196, App |
| 41 | 31 | 100.0 | 10 | 9 | US-09-881-490-197 Sequence 197, App |
| 42 | 31 | 100.0 | 10 | 9 | US-09-881-490-204 Sequence 204, App |
| 43 | 31 | 100.0 | 10 | 14 | US-10-006-557-11 Sequence 11, Appli |
| 44 | 31 | 100.0 | 10 | 15 | US-10-146-136-3 Sequence 3, Appli |
| 45 | 31 | 100.0 | 10 | 15 | US-10-146-136-5 Sequence 5, Appli |

ALIGNMENTS

RESULT 1
US-09-881-490-150
; Sequence 150, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; City: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94

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; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
;   NAME: McNicholas, Janet M.
;   REGISTRATION NUMBER: 32,918
;   REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 6 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: "XMP.317"
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: C-Terminus
;   OTHER INFORMATION: /label= Amidation
;   /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 150:
US-09-881-490-150
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Query Match          100.0%;   Score 31;   DB 9;   Length 6;
Best Local Similarity 100.0%;   Pred. No. 5.3e+05;
Matches 6;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;
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OY 1 LIQLFH 6
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Db 1 LIQLFH 6
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RESULT 2
US-09-765-527-175
; Sequence 175, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
;   APPLICANT: Better, Marc D.
;   TITLE OF INVENTION: Methods for Recombinant Microbial Production of
;                       Fusion Proteins and BPI-Derived Peptides
;   NUMBER OF SEQUENCES: 265
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;     STREET: 6300 Sears Tower, 233 South Wacker Drive
;     CITY: Chicago
;     STATE: Illinois
;     COUNTRY: United States of America
;     ZIP: 60606-6402
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/765,527
;     FILING DATE: 18-Jan-2001
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/521,803
;     FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Borun, Michael F.
;     REGISTRATION NUMBER: 25,447
;     REFERENCE/DOCKET NUMBER: 27129/33199
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 312/474-6300
;     TELEFAX: 312/474-0448
;     TELEX: 25-3856
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; INFORMATION FOR SEQ ID NO: 175:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 7 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: "XMP.309"
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: C-Terminus
;   OTHER INFORMATION: /label= Amidation
;   /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 175:
US-09-765-527-175

Query Match          100.0%;   Score 31;   DB 9;   Length 7;
Best Local Similarity 100.0%;   Pred. No. 5.3e+05;
Matches 6;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

OY 1 LIQLFH 6
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Db 2 LIQLFH 7

RESULT 3
US-09-765-527-176
; Sequence 176, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
;   APPLICANT: Better, Marc D.
;   TITLE OF INVENTION: Methods for Recombinant Microbial Production of
;                       Fusion Proteins and BPI-Derived Peptides
;   NUMBER OF SEQUENCES: 265
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;     STREET: 6300 Sears Tower, 233 South Wacker Drive
;     CITY: Chicago
;     STATE: Illinois
;     COUNTRY: United States of America
;     ZIP: 60606-6402
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/765,527
;     FILING DATE: 18-Jan-2001
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/621,803
;     FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Borun, Michael F.
;     REGISTRATION NUMBER: 25,447
;     REFERENCE/DOCKET NUMBER: 27129/33199
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 312/474-6300
;     TELEFAX: 312/474-0448
;     TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 176:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 7 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: "XMP.310"
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: C-Terminus
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? NAME/KEY: Modified-site
? LOCATION: C-Terminus
? OTHER INFORMATION: /label= Amidation
? /note= "The C-Terminus is Amidated"
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? SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-09-881-490-142

Query Match      100.0%; Score 31; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. NO. 5.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LIQLFH 6
        |||||
Db      2 LIQLFH 7

RESULT 5
US-09-881-490-143
: Sequence 143, Application US/09881490
: Patent No. US2002007298A1
: GENERAL INFORMATION:
: APPLICANT: Little II, Roger G.
: Lim, Edward
: Fadem, Mitchell B.
: TITLE OF INVENTION: Anti-Fungal Peptides
: NUMBER OF SEQUENCES: 211
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: McAndrews, Held & Malloy, Ltd.
: STREET: 500 West Madison Street, 34th FloorDrive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60661
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/881,490
: FILING DATE: 14-Jun-2001
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/119,858
: FILING DATE: <Unknown>
: APPLICATION NUMBER: 08/372,105
: FILING DATE: 13-JAN-95
: APPLICATION NUMBER: 08/306,473
: FILING DATE: 15-SEP-94
: APPLICATION NUMBER: 08/273,540
: FILING DATE: 11-JUL-94
: APPLICATION NUMBER: 08/209,762
: FILING DATE: 11-MAR-94
: APPLICATION NUMBER: 08/183,222
: FILING DATE: 14-JAN-94
: APPLICATION NUMBER: 08/093,202
: FILING DATE: 15-JUL-93
: APPLICATION NUMBER: 08/030,644
: FILING DATE: 12-MAR-93
: ATTORNEY/AGENT INFORMATION:
: NAME: McNicholas, Janet M.
: REGISTRATION NUMBER: 32,918
: REFERENCE/DOCKET NUMBER: 100-238/11021US01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/707-8889
: TELEFAX: 312/707-9155
: TELEX: 650 388-1248
: INFORMATION FOR SEQ ID NO: 143:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
:

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FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.310"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
/note= "The C-Terminus is Amidated."
SEQUENCE DESCRIPTION: SEQ ID NO: 143:
US-09-881-490-143

Query Match 100.0%; Score 31; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIQLFH 6
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Db 1 LIQLFH 6

RESULT 6
US-09-765-527-168
; Sequence 168, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.302"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 168:
US-09-765-527-168

Query Match 100.0%; Score 31; DB 9; Length 8;

Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LIQLFH 6
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Db 3 LIQLFH 8

RESULT 7
US-09-765-527-169
; Sequence 169, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.303"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 169:
US-09-765-527-169

Query Match 100.0%; Score 31; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIQLFH 6
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Db 2 LIQLFH 7

RESULT 8
US-09-765-527-170
; Sequence 170, Application US/09765527
; Patent No. US20020006638A1

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; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and Bpi-Derived Peptides
;
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.304"
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 170:
US-09-765-527-170

Query Match 100.0%; Score 31; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 1 LIQLFH 6

RESULT 9
US-09-881-490-135
; Sequence 135, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
;
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
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; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
;
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
;
; INFORMATION FOR SEQ ID NO: 135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.302"
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 135:
US-09-881-490-135

Query Match 100.0%; Score 31; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 3 LIQLFH 8

RESULT 10
US-09-881-490-136
; Sequence 136, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
;
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
```

CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/881,490
FILING DATE: 14-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/119,858
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/372,105
FILING DATE: 13-JAN-95
APPLICATION NUMBER: 08/306,473
FILING DATE: 15-SEP-94
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-94
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-94
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-94
APPLICATION NUMBER: 08/093,202
FILING DATE: 15-JUL-93
APPLICATION NUMBER: 08/030,644
FILING DATE: 12-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 100-238/11021US01
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.303"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
/note= "The C-terminus is Amidated"
SEQUENCE DESCRIPTION: SEQ ID NO: 136:
US-09-881-490-136
Query Match 100.0%; Score 31; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LIQLFH 6
Db 2 LIQLFH 7
RESULT 11
US-09-881-490-137
; Sequence 137, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/881,490
FILING DATE: 14-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/119,858
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/372,105
FILING DATE: 13-JAN-95
APPLICATION NUMBER: 08/306,473
FILING DATE: 15-SEP-94
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-94
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-94
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-94
APPLICATION NUMBER: 08/093,202
FILING DATE: 15-JUL-93
APPLICATION NUMBER: 08/030,644
FILING DATE: 12-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 100-238/11021US01
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.304"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
/note= "The C-terminus is Amidated"
SEQUENCE DESCRIPTION: SEQ ID NO: 137:
US-09-881-490-137
Query Match 100.0%; Score 31; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LIQLFH 6
Db 1 LIQLFH 6
RESULT 12
US-09-765-527-162
; Sequence 162, Application US/09765527
; Patent No. US2002006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of

```

;
; Fusion Proteins and HPI-Derived Peptides
;
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.296"
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated."
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-09-765-527-162

Query Match 100.0%; Score 31; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIQLFH 6
Db 4 LIQLFH 9

RESULT 13
US-09-765-527-163
; Sequence 163, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and Hpi-Derived Peptides
;
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.297"
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated."
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 163:
US-09-765-527-163

Query Match 100.0%; Score 31; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIQLFH 6
Db 3 LIQLFH 8

RESULT 14
US-09-765-527-164
; Sequence 164, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and HPI-Derived Peptides
;
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.298"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-09-765-527-164

Query Match 100.0%; Score 31; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIQLFH 6
Db 2 LIQLFH 7

RESULT 15
US-09-881-490-129
; Sequence 129, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Llm, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
```

```

;
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.296"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 129:
US-09-881-490-129

Query Match 100.0%; Score 31; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIQLFH 6
Db 4 LIQLFH 9

Search completed: October 14, 2003, 14:44:49
Job time : 15.625 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 ; Search time 7.875 Seconds
(without alignments)
73.271 Million cell updates/sec

Title: US-09-881-490-150

Perfect score: 31

Sequence: 1 LIQLFH 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 31 | 100.0 | 146 | 2 B86721 | transcription regul |
| 2 | 31 | 100.0 | 250 | 4 S43383 | bactericidal/perme |
| 3 | 31 | 100.0 | 487 | 2 A30909 | bactericidal/perme |
| 4 | 31 | 100.0 | 898 | 2 A98048 | H+/K+-exchanging A |
| 5 | 31 | 100.0 | 914 | 2 E95180 | cation-transportin |
| 6 | 30 | 96.8 | 1039 | 2 T30856 | protein F2 - Strep |
| 7 | 29 | 93.5 | 189 | 1 LPHUD | apolipoprotein D p |
| 8 | 29 | 93.5 | 313 | 2 S38538 | aspartoacylase - h |
| 9 | 29 | 93.5 | 370 | 2 D70076 | ethanolamine trans |
| 10 | 28 | 90.3 | 179 | 2 D83660 | hypoxanthine-guani |
| 11 | 28 | 90.3 | 212 | 2 S71432 | farnesyl-pyrophosp |
| 12 | 28 | 90.3 | 339 | 2 T42081 | farnesyl-pyrophosp |
| 13 | 28 | 90.3 | 347 | 2 T11664 | geranyltranstransi |
| 14 | 28 | 90.3 | 469 | 2 T51882 | hypothetical prote |
| 15 | 28 | 90.3 | 509 | 2 T32201 | hypothetical prote |
| 16 | 28 | 90.3 | 1277 | 2 S54451 | hypothetical prote |
| 17 | 28 | 90.3 | 2024 | 2 A54103 | centrosome autoant |
| 18 | 28 | 90.3 | 2301 | 2 T02323 | nodulin-like prote |
| 19 | 27 | 87.1 | 24 | 2 T42378 | phosphoprotein pho |
| 20 | 27 | 87.1 | 153 | 1 MYRB | myoglobin - rabbit |
| 21 | 27 | 87.1 | 159 | 2 E90327 | conserved hypothet |
| 22 | 27 | 87.1 | 213 | 2 D82849 | cell division prote |
| 23 | 27 | 87.1 | 324 | 2 T27302 | hypothetical prote |
| 24 | 27 | 87.1 | 343 | 2 T32173 | hypothetical prote |
| 25 | 27 | 87.1 | 357 | 2 T22879 | hypothetical prote |
| 26 | 27 | 87.1 | 357 | 2 T22880 | hypothetical prote |
| 27 | 27 | 87.1 | 359 | 2 T27200 | hypothetical prote |
| 28 | 27 | 87.1 | 360 | 2 T24641 | hypothetical prote |
| 29 | 27 | 87.1 | 478 | 2 S25821 | transposase - Baci |

30 27 87.1 478 2 C59095 hypothetical prote
31 27 87.1 499 1 A37924 heparin cofactor 1
32 27 87.1 648 2 T47988 serine/threonine-p
33 27 87.1 669 1 S62919 probable membrane
34 27 87.1 671 2 AE0486 probable membrane
35 27 87.1 716 2 H84421 probable receptor-
36 27 87.1 812 2 B97401 uridyltransferas
37 27 87.1 869 2 S68428 probable chloride
38 27 87.1 928 2 T24868 hypothetical prote
39 27 87.1 942 2 AB2619 hypothetical prote
40 27 87.1 1186 2 AG1928 two-component hybr
41 27 87.1 1822 2 S44849 K12H4.8 protein -
42 27 87.1 4196 2 T43274 dynein heavy chain
43 26 83.9 33 2 C86007 hypothetical prote
44 26 83.9 70 2 C90886 hypothetical prote
45 26 83.9 70 2 D85732 hypothetical prote

ALIGNMENTS

RESULT 1

B86721

transcription regulator [imported] - Lactococcus lactis subsp. lactis (strain IL1403
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: B86721

R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; E
Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lacti
A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: B86721

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-146 <STO>

A:Cross-references: GB:AE005176; PID:g12723688; PIDN:AAK04868.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: rnaG

Query Match 100.0%; Score 31; DB 2; Length 146;

Best Local Similarity 100.0%; Pred. No. 5.6;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIQLFH 6

|||||

Db 12 LIQLFH 17

RESULT 2

S43383

bactericidal/permeability-increasing protein - synthetic

C:Species: synthetic

A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

C:Date: 20-Oct-1994 #sequence_revision 15-Feb-1996 #text_change 15-Feb-1996

C:Accession: S43383

R:Qi, S.Y.; Li, Y.; C'Connor, C.D.

Biochem. J. 298, 711-718, 1994

A:Title: The region around residue 115 of human bactericidal/permeability-increasing
of a gene coding for the active domain and characterization of recombinant proteins.

A:Reference number: S43383

A:Accession: S43383

A:Molecule type: DNA

A:Residues: 1-250 <QIS>

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Best Local Similarity 100.0%; Score 31; DB 4; Length 250;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIQLFH 6

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Db 155 LIQLFH 160

RESULT 3

A30909
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N;Alternate names: 55K bactericidal protein
C;Species: Homo sapiens (man)
C;Date: 18-Apr-1989 #sequence_revision 18-Apr-1989 #text_change 20-Aug-1999
C;Accession: A33850; B54136; A29464; A43600; A49716; A30909
R;Gray, P.W.; Flagg, G.; Leong, S.R.; Gumina, R.J.; Weiss, J.; Ooi, C.F.; Elsbach, P.
J. Biol. Chem. 264, 9505-9509, 1989
A;Title: Cloning of the cDNA of a human neutrophil bactericidal protein. Structural and
A;Reference number: A33850; MUID:89255455; PMID:2722845
A;Accession: A33850
A;Molecule type: mRNA
A;Residues: 1-487 <GRA>
A;Cross-references: GHJ04739; NID:gl79528; PIDN:AA51841.1; PID:gl79529
R;Wilde, C.G.; Seilhamer, J.J.; McGrogan, M.; Ashton, N.; Shabie, J.L.; Lane, J.C.; Leon
J. Biol. Chem. 269, 17411-17416, 1994
A;Title: Bactericidal/permeability-increasing protein and lipopolysaccharide (LPS)-bindi
A;Reference number: A54136; MUID:94292492; PMID:7517398
A;Accession: B54136
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-374,'L',376-487 <WIL>
A;Experimental source: HL-60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:149855)
R;Ooi, C.F.; Weiss, J.; Elsbach, P.; Frangione, B.; Mannion, B.
J. Biol. Chem. 262, 14891-14894, 1987
A;Title: A 25-kDa amino-terminal fragment carries all the antibacterial activities of th
A;Reference number: A29464; MUID:88033057; PMID:3657613
A;Accession: A29464
A;Molecule type: protein
A;Residues: 32-51 <OOI>
A;Experimental source: neutrophils
R;Wasilik, K.R.; Skubitz, K.M.; Gray, B.H.
Infect. Immun. 59, 4193-4200, 1991
A;Title: Comparison of granule proteins from human polymorphonuclear leukocytes which an
A;Reference number: A43600; MUID:92040097; PMID:1937776
A;Accession: A43600
A;Molecule type: protein
A;Residues: 32-52,'R' <SWAS>
R;Little, R.G.; Kelner, D.N.; Lim, E.; Burke, D.J.; Conlon, P.J.
J. Biol. Chem. 269, 1865-1872, 1994
A;Title: Functional domains of recombinant bactericidal/permeability increasing protein
A;Reference number: A49716; MUID:94124531; PMID:8294435
A;Accession: A49716
A;Molecule type: protein
A;Residues: 32-130;132-141;143-165;202-215,'E',217-225 <LIT>
C;Comment: The bactericidal/permeability-increasing protein (BPI) is a 60 kD membrane-as
which is specific for gram-negative bacteria. BPI has a high affinity for lipopolysaccha
between BPI and an LPS-binding protein from liver and cholesterol ester transfer protein
C;Genetics:
A;Gene: GDB:BPI
A;Cross-references: GDB:131572; OMIM:109195
A;Map position: 20q11.23-20q12
C;Superfamily: lipopolysaccharide-binding protein
C;Keywords: antibacterial; cytotoxin; glycoprotein; heparin binding; neutrophil
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-487/Product: bactericidal permeability-increasing protein #status predicted <MAT>
F;32-51/Region: bactericidal #status predicted
F;380/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 31; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
|||||
DB 185 LIQLFH 190

RESULT 4

A98048

H+/K+-exchanging ATPase (EC 3.6.3.10) [imported] - Streptococcus pneumoniae (strain
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 19-Apr-2002
C;Accession: A98048
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Hargett, S.; DeHoff, B.S
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: A98048
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-898 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAL00214.1; PID:gl5459062; GSPDB:GN00174
C;Genetics:
A;Gene: pacL
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding dom
C;Keywords: hydrolase

Query Match 100.0%; Score 31; DB 2; Length 898;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
|||||
DB 806 LIQLFH 811

RESULT 5

E95180
cation-transporting ATPase, E1-E2 family SP1551 [imported] - Streptococcus pneumonia
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: E95180
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; I
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapp
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morri
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: E95180
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-914 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75638.1; PID:gl4973040; GSPDB:GN00164; TIGR
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1551
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding dom

Query Match 100.0%; Score 31; DB 2; Length 914;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
|||||
DB 822 LIQLFH 827

RESULT 6

T30856

protein F2 - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C;Accession: T30856
R;Jaffe, J.; Natanson-Yaron, S.; Caparon, M.G.; Hanski, E.
Mol. Microbiol. 21, 373-384, 1996
A;Title: Protein F2, a novel fibronectin-binding protein from Streptococcus pyogenes,
A;Reference number: 220907; MUID:97011581; PMID:8858591
A;Accession: T30856

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1039 <JAF>
A:Cross-references: EMBL:U31980; NID:g1654115; PID:g1654116; PIDN:AAC44522.1
C:Genetics:
A:Note: PRTF2

Query Match 96.8%; Score 30; DB 2; Length 1039;
Best Local Similarity 83.3%; Pred. No. 79;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
:|||||
Db 972 LVQLFH 977

RESULT 7
LPHUD
apolipoprotein D precursor [validated] - human
N:Alternate names: apod; gross cystic disease fluid protein 24 (GCDFP-24)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 *text_change 15-Sep-2000
C:Accession: A26958; A03224; S13050
R:Drayna, D.T.; McLean, J.W.; Wion, K.L.; Trent, J.M.; Drabkin, H.A.; Lawn, R.M.
DNA 6, 199-204, 1987
A:Title: Human apolipoprotein D gene: gene sequence, chromosome localization, and homolog
A:Reference number: A26958; MUID:87246069; PMID:2439269
A:Accession: A26958
A:Molecule type: DNA
A:Residues: 1-189 <DRA1>
A:Cross-references: GB:M16648; GB:M16649; GB:M16695; GB:M16696; NID:g178845; PIDN:AAA517
R:Drayna, D.; Fielding, C.; McLean, J.; Baer, B.; Castro, G.; Chen, E.; Comstock, L.; He
J. Biol. Chem. 261, 16535-16539, 1986
A:Title: Cloning and expression of human apolipoprotein D cDNA.
A:Reference number: A03224; MUID:87057347; PMID:3453108
A:Accession: A03224
A:Molecule type: mRNA
A:Residues: 1-189 <DRA2>
A:Cross-references: GB:J02611; NID:g178840; PIDN:AAH59517.1; PID:g178841
A:Note: part of the sequence was confirmed by protein sequencing
R:Balbin, M.; Freije, J.M.P.; Fucyo, A.; Sanchez, L.M.; Lopez-Otin, C.
Biochem. J. 271, 803-807, 1990
A:Title: Apolipoprotein D is the major protein component in cyst fluid from women with h
A:Reference number: S13050; MUID:91058519; PMID:2244881
A:Accession: S13050
A:Molecule type: protein
A:Residues: 28-41;42-45; 'X', 47-51;52-60;61-64, 'X', 66-73;76-82;83-97, 'X', 99-104;109-110, 'X'
A:Experimental source: mammary cyst fluid
A:Note: carbohydrate binding sites determined: the sequence of the amino-terminal pyrogl
R:Peitsch, M.C.; Boguski, M.S.
submitted to the Brookhaven Protein Data Bank, April 1992
A:Reference number: A50026; PDB:2APD
A:Contents: annotation; theoretical model, residues 21-189
R:Yang, C.Y.; Gu, Z.W.; Blanco-Vaca, F.; Gaskell, S.J.; Yang, M.; Massey, J.B.; Goltso Jn
Biochemistry 33, 12451-12455, 1994
A:Title: Structure of human apolipoprotein D: locations of the intermolecular and intram
A:Reference number: A55901; MUID:95001965; PMID:7918467
A:Contents: annotation; confirmation of peptide sequence overlap; disulfide bonds; N-gly
R:Schindler, P.A.; Settineri, C.A.; Collet, X.; Fielding, C.J.; Hurlingame, A.L.
Protein Sci. 4, 791-803, 1995
A:Title: Site-specific detection and structural characterization of the glycosylation of
pectrometry and sequential glycosidase digestion.
A:Reference number: A57914; MUID:95338133; PMID:7613477
A:Contents: annotation; N-glycosylation
C:Comment: Apod occurs in the macromolecular complex with lecithin-cholesterol acyltrans
C:Comment: Apod is primarily localized in HDL (60-65%), with most of the remainder in VH
C:Comment: Apod has been found in liver, intestine, pancreas, kidney, placenta, adrenal,
C:Genetics:
A:Gene: GDB:APOD
A:Cross-references: GDB:119690; OMIM:107740
A:Map position: 3q27-3qter
A:Introns: 41/3; 82/2; 112/1
A:Note: the first intron occurs before the initiator codon

C:Superfamily: lipocalin; lipocalin homology
C:Keywords: glycoprotein; lipid binding; lipid transport; lipoprotein; plasma; pyroc
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-189/Product: apolipoprotein D #status experimental <MAT>
F:37-185/Domain: lipocalin homology <LIP>
F:21/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status exper
F:28-134,61-185/Disulfide bonds: #status experimental
F:65,98/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:136/Disulfide bonds: interchain (to apolipoprotein A-II 29) #status experimental

Query Match 93.5%; Score 29; DB 1; Length 189;
Best Local Similarity 83.3%; Pred. No. 22;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
:|||||
Db 137 IIQLFH 142

RESULT 8
S38538
aspartoacylase - human
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1994 #sequence_revision 17-Nov-1995 *text_change 28-May-1999
C:Accession: S38538
R:Kaul, R.; Gao, G.P.; Balamurugan, K.; Matalon, R.
Nature Genet. 5, 118-123, 1993
A:Title: Cloning of the human aspartoacylase cDNA and a common missense mutation in
A:Reference number: S38538; MUID:94073185; PMID:8252036
A:Accession: S38538
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-313 <KAU>
A:Cross-references: GB:S67156; NID:g455833; PIDN:AAB29190.1; PID:g455834

Query Match 93.5%; Score 29; DB 2; Length 313;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
:|||||
Db 136 LIQMFH 141

RESULT 9
D70076
ethanolamine transporter homolog yxer - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 *text_change 15-Oct-1999
C:Accession: D70076
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Ga
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo,
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardir
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Ma
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scar
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; S
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiy
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshic
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtil
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D70076
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-370 <KUN>
A:Cross-references: GB:299124; GB:AL009126; NID:g2636442; PIDN:CAB15981.1; PID:el184
A:Experimental source: strain 168
C:Genetics:

A:Gene: yxer

Query Match 93.5%; Score 29; DB 2; Length 370;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6

|||||

Db 193 MIQLFH 198

RESULT 10

D83660

hypoxanthine-guanine phosphoribosyltransferase hprt [imported] - Bacillus halodurans (st

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: D83660

R:Takami, H.; Nakasone, K.; Takaki, Y.; Macino, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: D83660

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-179 <STO>

A:Cross-references: GB:AP001507; GB:BA000004; NID:gl0172612; PIDN:HA03803.1; GSPDR:GN00

A:Experimental source: strain C-125

C:Genetics:

A:Gene: hprt

C:Superfamily: hypoxanthine phosphoribosyltransferase

Query Match 90.3%; Score 28; DB 2; Length 179;

Best Local Similarity 83.3%; Pred. No. 35;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6

|||||

Db 110 LIELFH 135

RESULT 11

S71432

farnesyl-pyrophosphate synthetase - Sphaceloma manihoticola (fragment)

N:Alternate names: farnesyl-diphosphate synthase; farnesylpyrophosphate synthase

N:Contains: dimethylallyltransferase (EC 2.5.1.1); geranyltransferase (EC 2.5.

C:Species: Sphaceloma manihoticola

C:Date: 12-Mar-1998 #sequence_revision 12-Mar-1998 #text_change 20-Jun-2000

C:Accession: S71432

R:Homann, V.; Mende, K.; Arntz, C.; Ilardi, V.; Macino, G.; Morelli, G.; Boese, G.; Tudz

Curr. Genet. 30, 232-239, 1996

A:Title: The isoprenoid pathway: cloning and characterization of fungal FPPS genes.

A:Reference number: S71431; MUID:96337905; PMID:8753652

A:Accession: S71432

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-212 <HOM>

A:Cross-references: EMBL:X96941; NID:gl524344; PIDN:CAA65642.1; PID:gl524345

A:Experimental source: strain L1116

C:Genetics:

A:Gene: FPPS

C:Function:

A:Pathway: isoprenoid biosynthesis

C:Superfamily: farnesyl-pyrophosphate synthetase

C:Keywords: cytosol; dimer; isoprenoid biosynthesis; multifunctional enzyme; transferase

F:48-52/Region: DDXD motif

F:188-192/Region: DDXD motif

Query Match

Best Local Similarity 90.3%; Score 28; DB 2; Length 212;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6

|||||

Db 101 LIELFH 106

RESULT 12

T42081

farnesyl-pyrophosphate synthetase - fission yeast (Schizosaccharomyces pombe) (fragm

N:Contains: dimethylallyltransferase (EC 2.5.1.1); geranyltransferase (EC

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000

C:Accession: T42081

R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.

DNA Res. 4, 363-369, 1997

A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.

A:Reference number: Z17323; MUID:98162722; PMID:9501991

A:Accession: T42081

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-339 <YOS>

A:Cross-references: EMBL:D89104; NID:gl749415; PIDN:BAA13767.1; PID:gl749416

A:Experimental source: strain PR745

C:Function:

A:Description: catalyzes the sequential condensation of isopentenyl diphosphate with diphosphate with geranyl diphosphate forming farnesyl d

A:Pathway: isoprenoid biosynthesis

A>Note: first enzyme of isoprenoid biosynthesis

C:Superfamily: farnesyl-pyrophosphate synthetase

C:Keywords: isoprenoid biosynthesis; multifunctional enzyme; transferase

Query Match 90.3%; Score 28; DB 2; Length 339;

Best Local Similarity 83.3%; Pred. No. 69;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6

|||||

Db 133 LIELFH 138

RESULT 13

T1664

geranyltransferase (EC 2.5.1.10) - fission yeast (Schizosaccharomyces pombe)

N:Alternate names: farnesyl-diphosphate synthase

C:Species: Schizosaccharomyces pombe

C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 20-Jun-2000

C:Accession: T11664

R:Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, August 1997

A:Reference number: Z17305

A:Accession: T11664

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-347 <BAR>

A:Cross-references: EMBL:Z98533

C:Superfamily: farnesyl-pyrophosphate synthetase

C:Keywords: transferase

Query Match

Best Local Similarity 90.3%; Score 28; DB 2; Length 347;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6

|||||

Db 148 LIELFH 153

RESULT 14

T51882

hypothetical protein DKF2p547I194.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-2000

C:Accession: T51882

R:Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Weil, B.; Wiemann, S.

submitted to the Protein Sequence Database, July 2000

A:Reference number: Z25853

A;Accession: T51882
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 <AAA>
A;Cross-references: EMBL:AL390171
A;Experimental source: fetal brain; clone DKFZp547l194
C;Genetics:
A;Note: DKFZp547l194.1
C;Superfamily: Caenorhabditis elegans hypothetical protein F08C6.3

Query Match 90.3%; Score 28; DB 2; Length 469;
Best Local Similarity 83.3%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
|||:|
Db 427 LIQLYH 432

RESULT 15
T32201
hypothetical protein T02B11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32201
R;Goela, D.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid T02B11.
A;Reference number: 221135
A;Accession: T32201
A;Status: preliminary; translated from GB/EMBL/DCRJ
A;Molecule type: DNA
A;Residues: 1-509 <GCE>
A;Cross-references: EMBL:AF022979; PIDN:AAB69908.1; GSPDB:GN000023; CESP:T02B11.2
A;Experimental source: Strain Bristol N2; clone T02B11
C;Genetics:
A;Gene: CESP:T02B11.2
A;Map position: 5
A;Introns: 149/2; 171/3; 302/1; 316/1; 387/3; 497/1

Query Match 90.3%; Score 28; DB 2; Length 509;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
||:|
Db 313 LIQLFH 318

Search completed: October 14, 2003, 14:37:59
Job time : 10.875 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 ; Search time 4.25 Seconds
(without alignments)
66.391 Million cell updates/sec

Title: US-09-881-490-150
Perfect score: 31
Sequence: 1 LIQUFH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 31 | 100.0 | 483 | 1 BPI_HUMAN | P17213 homo sapien |
| 2 | 29 | 93.5 | 189 | 1 APOD_HUMAN | P05090 homo sapien |
| 3 | 29 | 93.5 | 313 | 1 ACY2_BOVIN | P46446 bos taurus |
| 4 | 29 | 93.5 | 313 | 1 ACY2_HUMAN | P45381 homo sapien |
| 5 | 29 | 93.5 | 370 | 1 YXER_BACSU | P54957 bacillus su |
| 6 | 28 | 90.3 | 347 | 1 FPPS_SCHPO | Q14230 schizosacch |
| 7 | 28 | 90.3 | 1277 | 1 PDS5_YEAST | Q04264 saccharomyc |
| 8 | 27 | 87.1 | 153 | 1 MYG_RABIT | P02170 oryctolagus |
| 9 | 27 | 87.1 | 359 | 1 RT22_MOUSE | Q9CWX2 mus musculu |
| 10 | 27 | 87.1 | 360 | 1 RT22_HUMAN | P82650 homo sapien |
| 11 | 27 | 87.1 | 416 | 1 PROA_LEPIN | P94872 leptospira |
| 12 | 27 | 87.1 | 478 | 1 T23E_BACTE | Q02403 bacillus th |
| 13 | 27 | 87.1 | 499 | 1 HEP2_HUMAN | P05546 homo sapien |
| 14 | 27 | 87.1 | 669 | 1 YNA8_YEAST | P53983 saccharomyc |
| 15 | 27 | 87.1 | 869 | 1 CLC6_HUMAN | P51797 homo sapien |
| 16 | 27 | 87.1 | 870 | 1 CLC6_MOUSE | O35454 mus musculu |
| 17 | 27 | 87.1 | 942 | 1 GLND_AGRTS | Q8UIF1 agrobacteri |
| 18 | 27 | 87.1 | 1845 | 1 DCR1_CAEEL | P34529 caenorhabdi |
| 19 | 27 | 87.1 | 4196 | 1 DYHC_SCHPO | Q13290 schizosacch |
| 20 | 26 | 83.9 | 101 | 1 SI07_BOVIN | Q28050 bos taurus |
| 21 | 26 | 83.9 | 151 | 1 RS15_PICMA | O65059 picea maria |
| 22 | 26 | 83.9 | 153 | 1 RS15_ELAOL | Q945U1 elaeis olei |
| 23 | 26 | 83.9 | 168 | 1 YPQE_BACSU | P50829 bacillus su |
| 24 | 26 | 83.9 | 206 | 1 Y187_PYRHO | O59533 pyrococcus |
| 25 | 26 | 83.9 | 289 | 1 YF03_PASMU | Q9CKV2 pasteurella |
| 26 | 26 | 83.9 | 304 | 1 LDCA_ECO57 | Q8XDJ8 escherichia |
| 27 | 26 | 83.9 | 304 | 1 LDCA_ECOL6 | P59238 escherichia |
| 28 | 26 | 83.9 | 304 | 1 LDCA_ECOL1 | P76008 escherichia |
| 29 | 26 | 83.9 | 309 | 1 FN3X_HUMAN | Q9HA64 homo sapien |
| 30 | 26 | 83.9 | 320 | 1 YC55_PORPU | P12003 porphyra pu |
| 31 | 26 | 83.9 | 349 | 1 FPPS_KLULA | P49349 kluyveromyc |
| 32 | 26 | 83.9 | 372 | 1 VGLI_HSV23 | P06764 herpes simp |
| 33 | 26 | 83.9 | 372 | 1 VGLI_HSV2H | P13291 herpes simp |

| | | | | | |
|----|----|------|------|--------------|--------------------|
| 34 | 26 | 83.9 | 506 | 1 PCCB_BACSU | P54541 bacillus su |
| 35 | 26 | 83.9 | 507 | 1 CDC7_YEAST | P06243 saccharomyc |
| 36 | 26 | 83.9 | 540 | 1 THI6_YEAST | P41835 s thiamine |
| 37 | 26 | 83.9 | 611 | 1 YJSL_YEAST | P46987 saccharomyc |
| 38 | 26 | 83.9 | 642 | 1 UL77_HCMVA | P16726 human cytom |
| 39 | 26 | 83.9 | 678 | 1 PTR3_YEAST | P43606 saccharomyc |
| 40 | 26 | 83.9 | 1257 | 1 CCAA_BACTU | Q45754 bacillus th |
| 41 | 26 | 83.9 | 1451 | 1 A2M2_MOUSE | P28666 mus musculu |
| 42 | 26 | 83.9 | 1476 | 1 A2M1_MOUSE | P28665 mus musculu |
| 43 | 26 | 83.9 | 2778 | 1 FAF_DROME | P55824 drosophila |
| 44 | 26 | 83.9 | 3655 | 1 YAMB_SCHPO | Q10064 schizosacch |
| 45 | 25 | 80.6 | 67 | 1 CD52_CANFA | Q28896 canis famil |

ALIGNMENTS

RESULT 1
BPI_HUMAN
ID BPI_HUMAN STANDARD; PRT; 483 AA.
AC P17213; Q9BY29; Q9H1L2; Q9H1M8; Q9H203; Q9UD65;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Bactericidal permeability-increasing protein precursor (BPI) (CAP 57).
GN BPI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-64.
RX MEDLINE=89255455; PubMed=2722846;
RA Gray P.W., Flaggs G., Leong S.R., Gumina R.J., Weiss J., Ooi C.E.,
RA Elsbach P.;
RT "Cloning of the cDNA of a human neutrophil bactericidal protein.
RT Structural and functional correlations.";
RL J. Biol. Chem. 264:9505-9509(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292492; PubMed=7517398;
RA Wilde C.G., Seilhamer J.J., McGrogan M., Ashton N., Snable J.L.,
RA Lane J.C., Leong S.R., Thornton M.B., Miller K.L., Scott R.W.;
RT "Bactericidal/permeability-increasing protein and lipopolysaccharide
RT (LPS)-binding protein. LPS binding properties and effects on LPS-
RT mediated cell activation.";
RL J. Biol. Chem. 269:17411-17416(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Xu J., Wang H.;
RT "Cloning of cDNA of human bactericidal/permeability-increasing
RT protein.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Symamre N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.,
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [5]
RP SEQUENCE OF 28-42.
RX MEDLINE=88033057; PubMed=3667613;
RA Ooi C.E., Weiss J., Elsbach P., Frangione B., Mannion B.;
RT "A 25-kDa NH2-terminal fragment carries all the antibacterial
RT activities of the human neutrophil 60-kDa
RT bactericidal/permeability-increasing protein.";
RL J. Biol. Chem. 262:14891-14894(1987).
RN [6]
RP SEQUENCE OF 28-47.
RX MEDLINE=89315847; PubMed=2501794;
RA Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,
RA Marra M.N., Seeger M., Nathan C.F.;
RT "Antibiotic proteins of human polymorphonuclear leukocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=97334442; PubMed=9186532;
RA Beamer L.J., Carroll S.F., Eisenberg D.;
RT "Crystal structure of human BPI and two bound phospholipids at 2.4-A
RT resolution.";
RL Science 276:1861-1864(1997).
CC -1- FUNCTION: THE CYTOTOXIC ACTION OF BPI IS LIMITED TO MANY SPECIES
CC OF GRAM-NEGATIVE BACTERIA; THIS SPECIFICITY MAY BE EXPLAINED BY A
CC STRONG AFFINITY OF THE VERY BASIC N-TERMINAL HALF FOR THE
CC NEGATIVELY CHARGED LIPOLYSACCHARIDES THAT ARE UNIQUE TO THE
CC GRAM-NEGATIVE BACTERIAL OUTER ENVELOPE.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED IN POLYMORPHONUCLEAR
CC LEUKOCYTES (PMN) GRANULES.
CC -1- TISSUE SPECIFICITY: RESTRICTED TO CELLS OF THE MYELOID SERIES.
CC -1- DOMAIN: THE N-TERMINAL REGION MAY BE EXPOSED TO THE INTERIOR OF
CC THE GRANULE, WHEREAS THE C-TERMINAL PORTION MAY BE EMBEDDED IN THE
CC MEMBRANE. DURING PHAGOCYTOSIS AND DEGRANULATION, PROTEASES MAY BE
CC RELEASED AND ACTIVATED AND CLEAVE BPI AT THE JUNCTION OF THE N-
CC AND C-TERMINAL PORTIONS OF THE MOLECULE, PROVIDING CONTROLLED
CC RELEASE OF THE N-TERMINAL ANTIBACTERIAL FRAGMENT WHEN BACTERIA ARE
CC INGESTED.
CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
CC -----
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CC -----
DR EMBL; J04739; AAA51841.1; ALT_INIT.
DR EMBL; AF322588; AAG42844.1; -.
DR EMBL; AL359555; CAC13043.1; -.
DR EMBL; AL499625; CAC27350.1; -.
DR EMBL; AL391692; CAC10453.1; -.
DR PDB; 1BP1; 04-SEP-97.
DR PDB; 1EWF; 21-JUN-00.
DR Genew; HGNC:1095; BPI.
DR MIM; 109195; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
DR PROSITE; PS00400; LBP_BPI_CETP; 1.

KW Antibiotic; Signal; Transmembrane; Glycoprotein; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 483
FT SITE 236 241
FT TRANSMEM 365 385
FT CONFLICT 12 12
FT CONFLICT 212 212
FT CONFLICT 351 351
FT CONFLICT 371 371
FT CONFLICT 400 400
FT CONFLICT 407 407
FT STRAND 32 37
FT HELIX 38 56
FT TURN 57 58
FT STRAND 64 70
FT TURN 71 73
FT STRAND 74 89
FT STRAND 93 98
FT TURN 99 101
FT STRAND 102 122
FT TURN 123 124
FT STRAND 125 149
FT TURN 150 153
FT STRAND 154 163
FT STRAND 168 172
FT TURN 174 175
FT HELIX 179 188
FT TURN 189 189
FT HELIX 190 217
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FT STRAND 223 225
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FT STRAND 236 236
FT STRAND 241 242
FT STRAND 246 251
FT STRAND 254 257
FT STRAND 281 286
FT HELIX 287 299
FT TURN 300 301
FT STRAND 304 307
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FT STRAND 321 321
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FT HELIX 332 335
FT STRAND 340 347
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FT STRAND 359 363
FT STRAND 365 373
FT TURN 375 376
FT STRAND 379 388
FT STRAND 391 398
FT TURN 399 400
FT STRAND 401 408
FT STRAND 412 412
FT TURN 415 418
FT TURN 419 420
FT HELIX 425 428
FT HELIX 429 450
FT STRAND 452 453
FT TURN 458 459
FT STRAND 460 470
FT TURN 471 472
FT STRAND 473 483
SQ SEQUENCE 483 AA; 53396 MW; AD58C92BCAD8F47C CRC64;

Query Match 100.0%; Score 31; DB 1; Length 483;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LIQLFH 6
Db      |||||
        181 LIQLFH 186

RESULT 2
APOD_HUMAN
ID      APOD_HUMAN      STANDARD:      PRT:      189 AA.
AC      P05090;
DT      13-AUG-1987 (Rel. 05, Created)
DT      13-AUG-1987 (Rel. 05, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Apolipoprotein D precursor (Apo-D) (APOD).
GN      APOD.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=87057347; PubMed=3453108;
RA      Drayna D.T., Fielding C., McLean J.W., Baer B., Castro G., Chen E.,
RA      Comstock L., Henzel W., Kohr W., Rhee L., Wion K.L., Lawn R.M.;
RT      "Cloning and expression of human apolipoprotein D cDNA.";
RL      J. Biol. Chem. 261:16535-16539(1986).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=87246069; PubMed=2439269;
RA      Drayna D.T., McLean J.W., Wion K.L., Trent J.M., Drabkin H.A.,
RA      Lawn R.M.;
RT      "Human apolipoprotein D gene: gene sequence, chromosome localization,
RT      and homology to the alpha 2u-globulin superfamily.";
RL      DNA 6:199-204(1987).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Skin;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length
RT      human and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [4]
RP      SEQUENCE OF 21-189, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RC      TISSUE=Plasma;
RX      MEDLINE=95001965; PubMed=7918467;
RA      Yang C.-Y., Gu Z.-W., Blanco-Vaca F., Gaskell S.J., Yang M.,
RA      Massey J.B., Gatto A.M. Jr., Pownall H.J.;
RT      "Structure of human apolipoprotein D: locations of the intermolecular
RT      and intramolecular disulfide links.";
RL      Biochemistry 33:12451-12455(1994).
RN      [5]
RP      SEQUENCE OF 92-189 FROM N.A.
RC      TISSUE=Lacrimal gland;
RX      MEDLINE=96148565; PubMed=8549691;
RA      Holzfeind P., Merschak P., Dieplinger H., Redl B.;
RT      "The human lacrimal gland synthesizes apolipoprotein D mRNA in
RT      addition to tear prealbumin mRNA, both species encoding members of
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RT      the lipocalin superfamily.";
RT      Exp. Eye Res. 61:495-500(1995).
RN      [6]
RP      PARTIAL SEQUENCE OF 128-187.
RX      MEDLINE=91058519; PubMed=2244881;
RA      Balbin M., Freije J.M.P., Fueyo A., Sanchez L.M., Lopez-Otin C.;
RT      "Apolipoprotein D is the major protein component in cyst fluid from
RT      women with human breast gross cystic disease.";
RL      Biochem. J. 271:803-807(1990).
RN      [7]
RP      3D-STRUCTURE MODELING, AND BILIN-BINDING.
RX      MEDLINE=91190834; PubMed=2083249;
RA      Peitsch M.C., Boguski M.S.;
RT      "Is apolipoprotein D a mammalian bilin-binding protein?";
RL      New Biol. 2:197-206(1990).
RN      [8]
RP      CARBOHYDRATE-LINKAGE SITES.
RX      MEDLINE=95338133; PubMed=7613477;
RA      Schindler P.A., Settineri C.A., Coillet X., Fielding C.J.,
RA      Burlingame A.L.;
RT      "Site-specific detection and structural characterization of the
RT      glycosylation of human plasma proteins lecithin:cholesterol
RT      acyltransferase and apolipoprotein D using HPLC/electrospray mass
RT      spectrometry and sequential glycosidase digestion.";
RL      Protein Sci. 4:791-803(1995).
RN      [9]
RP      VARIANTS SER-15; ILEU-115 AND LYS-178.
RX      MEDLINE=99318093; PubMed=10391209;
RA      Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA      Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
RA      Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
RA      Lander E.S.;
RT      "Characterization of single-nucleotide polymorphisms in coding regions
RT      of human genes.";
RL      Nat. Genet. 22:231-238(1999).
RN      [10]
RP      ERRATUM.
RA      Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA      Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
RA      Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
RA      Lander E.S.;
RL      Nat. Genet. 23:373-373(1999).
CC      -1- FUNCTION: APOD OCCURS IN THE MACROMOLECULAR COMPLEX WITH LECITHIN-
CC      CHOLESTEROL ACYLTRANSFERASE. IT IS PROBABLY INVOLVED IN THE
CC      TRANSPORT AND BINDING OF BILIN. APPEARS TO BE ABLE TO TRANSPORT A
CC      VARIETY OF LIGANDS IN A NUMBER OF DIFFERENT CONTEXTS.
CC      -1- SUBUNIT: Homodimer. In plasma, also exists as a disulfide-linked
CC      heterodimer with APOA2.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- TISSUE SPECIFICITY: Expressed in liver, intestine, pancreas,
CC      kidney, placenta, adrenal, spleen, fetal brain tissue and tears.
CC      -1- MISCELLANEOUS: APOD IS PRIMARILY LOCALIZED IN HDL (60-65%), WITH
CC      MOST OF THE REMAINDER IN VHDL AND ONLY TRACE AMOUNTS IN VLDL AND
CC      LDL.
CC      -1- SIMILARITY: Belongs to the lipocalin family.
CC      -----
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CC      -----
CC      EMBL: J02611; AAB59517.1; -.
CC      EMBL: M16596; AAA51764.1; -.
CC      EMBL: BC007402; AAH07402.1; -.
CC      EMBL: S80440; AAB35919.1; -.
CC      PIR: A26958; LPHUD.
CC      PDB: 2APD; 15-OCT-94.
CC      SWISS-2DPAGE; P05090; HUMAN.
CC      Genew; HGNC:612; APOD.
CC      MIM: 107740; -.
DR      EMBL: J02611; AAB59517.1; -.
DR      EMBL: M16596; AAA51764.1; -.
DR      EMBL: BC007402; AAH07402.1; -.
DR      EMBL: S80440; AAB35919.1; -.
DR      PIR: A26958; LPHUD.
DR      PDB: 2APD; 15-OCT-94.
DR      SWISS-2DPAGE; P05090; HUMAN.
DR      Genew; HGNC:612; APOD.
DR      MIM: 107740; -.

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DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005321; F:high-density lipoprotein; TAS.
DR GO; GO:0006629; P:lipid metabolism; TAS.
DR InterPro: IPR002345; Lipocalin.
DR InterPro: IPR000566; Lipocalin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00179; LIPOCALIN.
DR PROSITE; PS00213; LIPOCALIN; 1.
KW Glycoprotein; Plasma; Lipid-binding; Transport; Signal; Lipocalin;
KW 3D-structure; Polymorphism; Pyrrolidone carboxylic acid.
FT SIGNAL 1 20
FT CHAIN 21 189 APOLIPOPROTEIN D.
FT MOD_RES 21 21 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 28 134
FT DISULFID 61 185
FT DISULFID 136 136
FT CARBOHYD 65 65
FT CARBOHYD 98 98
FT VARIANT 15 15
FT VARIANT 115 115
FT VARIANT 178 178
FT STRAND 23 25
FT HELIX 39 42
FT STRAND 44 51
FT HELIX 55 57
FT STRAND 60 67
FT TURN 70 71
FT STRAND 75 81
FT TURN 84 85
FT STRAND 87 96
FT STRAND 103 107
FT STRAND 109 109
FT TURN 110 111
FT STRAND 112 112
FT STRAND 115 123
FT STRAND 128 137
FT TURN 138 140
FT STRAND 141 150
FT HELIX 157 167
FT HELIX 174 176
FT STRAND 178 179
SQ SEQUENCE 189 AA; 21275 MW; 0EAA6DE03D5E71A8 CRC64;

Query Match 93.5%; Score 29; DB 1; Length 189;
Best Local Similarity 83.3%; Pred. NO. 8.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 137 IIQLFH 142

RESULT 3
ID ACY2_BOVIN STANDARD; PRT; 313 AA.
AC P46446;
DT 01-NOV-1995 (Rel. 32, Created)
DI 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Aspartoacylase (EC 3.5.1.15) (Aminoacylase-2) (ACY-2).
GN ASPA OR ACY2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=94073185; PubMed=8252036;

RA Kaul R., Gao G.P., Balamurugan K., Matalon R.;
RT "Cloning of the human aspartoacylase cDNA and a common missense
RT mutation in Canavan disease.";
RL Nat. Genet. 5:118-123(1993).
CC -1- FUNCTION: RESPONSIBLE FOR THE CLEAVAGE OF N-ACETYLASPARTIC ACID
CC WHICH OCCURS IN HIGH CONCENTRATION IN BRAIN.
CC -1- CATALYTIC ACTIVITY: N-acyl-L-aspartate + H(2)O - a fatty acid
CC anion + L-aspartate.
CC -1- SIMILARITY: TO HUMAN ASPARTOACYLASE.
CC -----
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CC -----
CC EMBL; S74726; AAD14980.1; .
DR InterPro: IPR007036; Aste_Aspa.
DR Pfam; PF04952; Aste_Aspa; 1.
KW Hydrolase.
FT ACT_SITE 21 21 POTENTIAL.
FT ACT_SITE 285 285 POTENTIAL.
SQ SEQUENCE 313 AA; 35738 MW; 1414D37921891009 CRC64;

Query Match 93.5%; Score 29; DB 1; Length 313;
Best Local Similarity 83.3%; Pred. NO. 15;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 136 LIQMFH 141

RESULT 4
ID ACY2_HUMAN STANDARD; PRT; 313 AA.
AC P45381;
DT 01-NOV-1995 (Rel. 32, Created)
DI 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Aspartoacylase (EC 3.5.1.15) (Aminoacylase-2) (ACY-2).
GN ASPA OR ASP OR ACY2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT CD ALA-285.
RC TISSUE=Kidney;
RX MEDLINE=94073185; PubMed=8252036;
RA Kaul R., Gao G.P., Balamurugan K., Matalon R.;
RT "Cloning of the human aspartoacylase cDNA and a common missense
RT mutation in Canavan disease.";
RL Nat. Genet. 5:118-123(1993).
RN [2]
RP VARIANTS CD ALA-285 AND GLU-305.
RX MEDLINE=94295593; PubMed=8023850;
RA Kaul R., Gao G.P., Aloya M., Balamurugan K., Petrosky A., Michals K.,
RA Matalon R.;
RT "Canavan disease: mutations among Jewish and non-jewish patients.";
RL Am. J. Hum. Genet. 55:34-41(1994).
RN [3]
RP VARIANTS CD 176-GLY-ILE-177 DEL; ARG-274; SER-295 AND GLU-305.
RX MEDLINE=95397842; PubMed=7668285;
RA Shaag A., Anikster Y., Christensen E., Glustein J.2., Pois A.,
RA Michelakakis H., Nigro F., Pronicka E., Ribes A., Zabot M.-T.,
RA Elpeleg O.N.;
RT "The molecular basis of canavan (aspartoacylase deficiency) disease
RT in European non-Jewish patients.";
RL Am. J. Hum. Genet. 57:572-580(1995).
RN [4]

RP VARIANT CD ARG-152.
RX MEDLINE-95322986; PubMed=7599639;
RA Kaul R., Gao G.P., Michaels K., Whelan D.S., Levin S., Matalon R.;
RT "Novel (Cys152>Arg) missense mutation in an Arab patient with
RT Canavan disease.";
RL Hum. Mutat. 5:269-271(1995).
RN [5]
RP VARIANT CD THR-143.
RX MEDLINE-98112496; PubMed-9452117;
RA Kobayashi K., Tsujino S., Ezoe F., Hamaguchi H., Nihei K.,
RA Sakuragawa N.;
RT "Missense mutation (I143T) in a Japanese patient with Canavan
RT disease.";
RL Hum. Mutat. Suppl. 1:S308-S309(1998).
CC -!- FUNCTION: RESPONSIBLE FOR THE CLEAVAGE OF N-ACETYLSPARTIC ACID
CC (NAA) WHICH OCCURS IN HIGH CONCENTRATION IN BRAIN. HYDROLYSIS OF
CC NAA PLAYS A SIGNIFICANT PART IN THE MAINTENANCE OF INTACT WHITE
CC MATTER. IN OTHER TISSUES ACTS AS A SCAVENGER OF NAA FROM BODY
CC FLUIDS.
CC -!- CATALYTIC ACTIVITY: N-acyl-L-aspartate + H(2)O -> a fatty acid
CC anion + L-aspartate.
CC -!- TISSUE SPECIFICITY: BRAIN WHITE MATTER, SKELETAL MUSCLE, KIDNEY,
CC ADRENAL GLANDS, LUNG AND LIVER.
CC -!- DISEASE: Defects in ASPA are the cause of Canavan disease (CD),
CC also known as spongy degeneration of the brain. CD is an autosomal
CC recessive leukodystrophy clinically characterized by atonia of
CC neck muscles, hyperextension of legs and flexion of arms,
CC blindness, severe mental defect, megaloccephaly, and death by 18
CC months on the average.
CC -!- SIMILARITY: TO BOVINE ASPARTOACYLASE.
CC -----
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CC -----
DR EMBL; S67156; AAB29190.1; -.
DR PIR; S38538; S38538.
DR Genew; HGNC:756; ASPA.
DR MIM; 271900; -.
DR GO; GO:0004046; F:aminoacylase activity; TAS.
DR GO; GO:0006533; P:aspartate catabolism; TAS.
DR InterPro; IPR007036; Aste_Aspa.
DR Pfam; PF04952; Aste_Aspa; 1.
KW Hydrolase; Disease mutation.
FT ACT_SITE 21 21 POTENTIAL.
FT ACT_SITE 285 285 POTENTIAL.
FT VARIANT 143 143 I -> T (IN CD; IN A JAPANESE PATIENT).
FT VARIANT 152 152 /FTid-var_004995.
FT VARIANT 176 177 C -> R (IN CD; LOSS OF ACTIVITY).
FT VARIANT 176 177 /FTid-var_004996.
FT VARIANT 274 274 MISSING (IN CD).
FT VARIANT 274 274 /FTid-var_004997.
FT VARIANT 274 274 G -> R (IN CD).
FT VARIANT 285 285 /FTid-var_004998.
FT VARIANT 285 285 E -> A (IN CD; 2.5% OF ACTIVITY;
FT PREDOMINANT MUTATION IN ASHKENAZI JEWISH
FT POPULATION).
FT VARIANT 295 295 /FTid-var_004999.
FT VARIANT 295 295 F -> S (IN CD).
FT VARIANT 305 305 /FTid-var_005000.
FT VARIANT 305 305 A -> E (IN CD; LOSS OF ACTIVITY; PAN-
FT EUROPEAN ORIGIN; MOST PREVALENT AMONG
FT NON-JEWISH CD PATIENTS; PROBABLY THE MOST
FT ANCIENT MUTATION).
FT /FTid-var_005001.
SQ SEQUENCE 313 AA; 35735 MW; 33C0B9B07839E7F5 CRC64;
Query Match 93.5%; Score 29; DB 1; Length 313;
Best Local Similarity 83.3%; Pred. No. 15;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LIQLPH 6
Db 136 LIQMFH 141
RESULT 5
YXER_BACSU STANDARD; PRT; 370 AA.
AC P54957;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yxer.
GN YXER OR LP6A.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
KP SEQUENCE FROM N.A.
RC STRAIN=168 / BGSC1A1;
RX MEDLINE-97021444; PubMed=8867804;
RA Yoshida K.-I., Fujimura M., Yanai N., Fujita Y.;
RT "Cloning and sequencing of a 23-kb region of the Bacillus subtilis
RT genome between the *iol* and *hut* operons.";
RL DNA Res. 2:295-301(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE-98044033; PubMed-9384377;
RA Kunst P., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gaizizi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinio S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -!- SIMILARITY: TO S.TYPHIMURIUM ETHANOLAMINE UTILIZATION PROTEIN
CC EUTH.
CC -----
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CC EMBL; D45912; BAA08334.1; -.
DR EMBL; 299124; CAB15981.1; -.
DR PIR; D70076; D70076.
DR Subtilist; BG11894; yxeR.
DR Pfam; PF04346; EucH; 1.
KW Hypothetical protein; Transmembrane; Transport; Complete proteome.
FT TRANSMEM 6 26 POTENTIAL.
FT TRANSMEM 49 69 POTENTIAL.
FT TRANSMEM 79 99 POTENTIAL.
FT TRANSMEM 111 131 POTENTIAL.
FT TRANSMEM 143 163 POTENTIAL.
FT TRANSMEM 167 187 POTENTIAL.
FT TRANSMEM 206 226 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT TRANSMEM 307 327 POTENTIAL.
FT TRANSMEM 333 353 POTENTIAL.
SQ SEQUENCE 370 AA; 38414 MW; E7BF1585EB600DF8 CRC64;

Query Match 93.5%; Score 29; DB 1; Length 370;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 193 MIQLFH 198

RESULT 6
FPPS_SCHPO STANDARD; PRT; 347 AA.
ID FPPS_SCHPO
AC O14230; F78756;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable farnesyl pyrophosphate synthetase (FPP synthetase) (FPPS)
DE (Farnesyl diphosphate synthetase) [includes: dimethylallyltransferase
DE (EC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10)].
GN SPAC6F12.13C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam K., Rajandream M.A., Lyne M., Iyne R., Stewart A.,
RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welltjens I., Vanstreels E., Rieger M., Schaefer-M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moest D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Carzon A., Thode C.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RA *The genome sequence of Schizosaccharomyces pombe.*;
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RL Nature 415:871-880(2002).
RN [2]
RP SEQUENCE OF 16-347 FROM N.A.
RC STRAIN=PR745;
RX MEDLINE=98162722; PubMed=9501991;
RA Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
RT *Identification of open reading frames in Schizosaccharomyces pombe
RT cDNAs.*;
RL DNA Res. 4:363-369(1997).
CC -!- FUNCTION: CATALYZES THE SEQUENTIAL CONDENSATION OF ISOPENTENYL
CC PYROPHOSPHATE WITH THE ALLYLIC PYROPHOSPHATES, DIMETHYLALLYL
CC PYROPHOSPHATE, AND THEN WITH THE RESULTANT GERANYLPYROPHOSPHATE
CC TO THE ULTIMATE PRODUCT FARNESYL PYROPHOSPHATE.
CC -!- CATALYTIC ACTIVITY: Dimethylallyl diphosphate + isopentenyl
CC diphosphate = diphosphate + geranyl diphosphate.
CC -!- CATALYTIC ACTIVITY: Geranyl diphosphate + isopentenyl diphosphate
CC = diphosphate + trans,trans-farnesyl diphosphate.
CC -!- PATHWAY: ISOPRENE BIOSYNTHESIS, CHOLESTEROL BIOSYNTHESIS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE FPP/GGPP SYNTHETASES FAMILY.
CC -----
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CC -----
DR EMBL; Z98533; CAB11097.1; -.
DR EMBL; D89104; BAA13767.1; -.
DR PIR; I11664; T11664.
DR HSSP; P08836; 1FPS.
DR GeneDB_SPombe; SPAC6F12.13C; -.
DR InterPro; IPR000092; Polyprenyl_synt.
DR Pfam; PF00348; polyprenyl_synt; 1.
DR PROSITE; PS00723; POLYPRENYL_SYNTHET_1; 1.
DR PROSITE; PS00444; POLYPRENYL_SYNTHET_2; 1.
KW Transferase; Isoprene biosynthesis; Cholesterol biosynthesis.
FT ACT_SITE 184 184 BY SIMILARITY.
FT CONFLICT 203 203 A -> E (IN REF. 2).
FT CONFLICT 346 347 NK -> ISKFLVLCF (IN REF. 2).
SQ SEQUENCE 347 AA; 39516 MW; 483029A5FC15B9F5 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 347;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 148 LIQLFH 153

RESULT 7
PDS5_YEAST
ID PDS5_YEAST STANDARD; PRT; 1277 AA.
AC Q04264; Q04780;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sister chromatid cohesion protein PDS5 (precocious dissociation of
DE sisters protein 5).
GN PDS5 OR YMR076C OR YM9582.01C OR YM9916.15C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
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RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.,
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
XIII.",
RL Nature 387:90-93(1997).
RN [2]
RP FUNCTION, AND SUBCELLULAR LOCATION.
RX MEDLINE=20517447; PubMed=11062262;
RA Hartman T., Stead K., Koshland D., Guacci V.,
RT "Pds5p is an essential chromosomal protein required for both sister
chromatid cohesion and condensation in Saccharomyces cerevisiae.",
RL J. Cell Biol. 151:613-625(2000).
RN [3]
RP FUNCTION.
RX MEDLINE=21065936; PubMed=11137006;
RA Panizza S., Tanaka T., Hochwagen A., Eisenhaber F., Nasmyth K.,
RT "Pds5 cooperates with cohesin in maintaining sister chromatid
cohesion.",
RL Curr. Biol. 10:1557-1564(2000).
CC -!- FUNCTION: Essential for the establishment and maintenance of
CC sister chromatid cohesion at centromere proximal and distal
CC regions during S phase. Also required for chromosomal
CC condensation.
CC -----
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CC -----
DR EMBL; Z49259; CAA89222.1; -;
DR EMBL; Z48952; CAA88801.1; -;
DR PIR; S54451; S54451.
DR SGD; S0004581; PDS5.
DR GO; GO:0005708; C:mitotic chromosome; IDA.
DR GO; GO:0007076; P:mitotic chromosome condensation; IMP.
DR GO; GO:0007064; P:mitotic sister chromatid cohesion; IMP.
KW Mitosis; Nuclear protein.
SQ SEQUENCE 1277 AA; 147040 MW; 9DF40A5274FD9623 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 1277;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
||:||||
Db 149 LIQLFH 154

RESULT 8
MYG_RABIT
ID MYG_RABIT STANDARD; PRT; 153 AA.
AC P02170;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myoglobin.
GN MB.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=76253773; PubMed=952958;
RA Romero-Herrera A.E., Lehmann H., Castillo O.,
RT "The primary structure of the myoglobin of rabbit (Oryctolagus
RT cuniculus).",
RL Biochim. Biophys. Acta 439:51-54(1976).
CC -!- FUNCTION: SERVES AS A RESERVE SUPPLY OF OXYGEN AND FACILITATES
CC THE MOVEMENT OF OXYGEN WITHIN MUSCLES.

CC -!- SIMILARITY: Belongs to the globin family.
DR PIR; A02492; MYRB.
DR HSSP; P02189; IMWC.
DR InterPro; IPR000971; Globin.
DR InterPro; IPR002335; Myoglobin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00613; MYOGLOBIN.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Muscle.
FT METAL 64 64 IRON (HEME DISTAL LIGAND).
FT METAL 93 93 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 153 AA; 17089 MW; D77CE1301269EB1F CRC64;

Query Match 87.1%; Score 27; DB 1; Length 153;
Best Local Similarity 83.3%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
||:||||
Db 29 LIQLFH 34

RESULT 9
RT22_MOUSE
ID RT22_MOUSE STANDARD; PRT; 359 AA.
AC Q9CXW2; Q8VVG9; Q9DL85;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Mitochondrial 28S ribosomal protein S22 (S22mt) (MRP-S22).
GN MRPS22 OR RPM22.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo, and Embryonic head;
RX PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaesterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.",
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE OF 254-359 FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary gland;
RX PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
CC -----
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CC -----
DR EMBL; AK003836; BAH23027.2; -;
DR EMBL; AK013925; BAH29061.1; -;
DR EMBL; BC021882; AAH21882.1; ALT_INIT.
DR MGD; MGI:1928137; Mrps22.
KW Ribosomal protein; Mitochondrion.
SQ SEQUENCE 359 AA; 41192 MW; C258AD152738F1C7 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 359;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 299 LVQLYH 304
|:|:|:

RESULT 10
RT22_HUMAN STANDARD; PRT; 360 AA.
ID RT22_HUMAN
AC P82650;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Mitochondrial 28S ribosomal protein S22 (S22mt) (MRP-S22) (GK002).
GN MRPS22 OR RPSM22 OR C3ORF5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver cancer;
RA Li Y., Wu T., Xu S., Ren S., Chen Z., Han Z.;
RT "A novel gene expressed in human liver cancer tissue.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21096975; PubMed=11175783;
RA Crisponi L., Deliana M., Loi A., Chiappe F., Uda M., Amati P.,
RA Bisceglia L., Zelante L., Nagaraja R., Porcu S., Ristaldi M.S.,
RA Marzella R., Rocchi M., Nicolino M., Lienhardt-Roussie A., Nivelon A.,
RA Verloes A., Schlessinger D., Gasparini P., Bonneau D., Cao A.,

RA Pilia G.;
RT "The putative forkhead transcription factor FOXL2 is mutated in
RT blepharophimosis/ptosis/epicanthus inversus syndrome.";
RL Nat. Genet. 27:159-166(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP IDENTIFICATION.
RX MEDLINE=20490686; PubMed=10938081;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Koc H.,
RA Spemullil L.L.;
RT "A proteomics approach to the identification of mammalian
RT mitochondrial small subunit ribosomal proteins.";
RL J. Biol. Chem. 275:32585-32591(2000).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF226045; AAF86945.1; -;
DR EMBL; AF321613; AAK01406.1; -;
DR EMBL; BC009296; AAH09296.1; -;
DR Genew; HGNC:14508; MRPS22.
DR MIM; 605810; -;
DR GO; GO:0005761; C:mitochondrial ribosome; NAS.
KW Ribosomal protein; Mitochondrion.
SQ SEQUENCE 360 AA; 41280 MW; 2DB50257C222D706 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 360;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 300 LVQLYH 305
|:|:|:

RESULT 11
PROA_LEPIN STANDARD; PRT; 416 AA.
ID PROA_LEPIN
AC P94872;
DT 30-MAY-2000 (Rel. 39, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-semialdehyde dehydrogenase) (Glutamyl-gamma-semialdehyde dehydrogenase) (GSA dehydrogenase).
GN PROA OR LA0854.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiaceae; Leptospira.
OX NCBI_TaxID-173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Serotype 2;
RX MEDLINE-22598143; PubMed-12712204;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H., Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F., Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F., Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W., Yao Z.-J., Shen Y., Qiang H.-Q., Xia Q.-C., Guo X.-K., Danchin A., Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z., Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
CC -!- FUNCTION: CATALYZES THE NADPH DEPENDENT REDUCTION OF L-GAMMA-GLUTAMYL 5-PHOSPHATE INTO L-GLUTAMATE 5-SEMIALDEHYDE AND PHOSPHATE. THE PRODUCT SPONTANEOUSLY UNDERGOES CYCLIZATION TO FORM 1-PYRROLINE-5-CARBOXYLATE.
CC -!- CATALYTIC ACTIVITY: L-glutamate 5-semialdehyde + phosphate + NADP(+) = L-gamma-glutamyl 5-phosphate + NADPH.
CC -!- PATHWAY: Proline biosynthesis; second step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE GAMMA-GLUTAMYL PHOSPHATE REDUCTASE FAMILY.
CC -----
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CC -----
DR EMBL; U73651; AAB39854.1; -.
DR EMBL; AE011270; AAM48053.1; -.
DR HAMAP; MF_00412; -. 1.
DR InterPro; IPR002086; Adehyde_dehydr.
DR InterPro; IPR000965; Gglut_pp_reduct.
DR Pfam; PF00171; ailedh; 1.
DR TIGRFAMs; TIGR00407; proA; 1.
DR PROSITE; PS01223; PROA; FALSE_NEG.
KW Oxidoreductase; Proline biosynthesis; NADP: Complete proteome.
FT CONFLICT 32 32 V -> I (IN REF. 1).
FT CONFLICT 299 299 N -> K (IN REF. 1).
FT CONFLICT 305 305 E -> Q (IN REF. 1).
SQ SEQUENCE 416 AA; 45768 MW; A949288589EB0B9A CRC64;

Query Match 87.1%; Score 27; DB 1; Length 416;
Best Local Similarity 83.3%; Pred.No. 61;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
||:|
Db 160 LIKLFH 165

RESULT 12
T23E_BACTF STANDARD; PRT; 478 AA.
AC Q02403;
DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transposase for insertion sequence element IS231E.
OS Bacillus thuringiensis (subsp. finitimus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID-29337;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Serotype 2;
RX MEDLINE-92374847; PubMed-1324390;
RA Ressochazy R., Hallet B., Delcour J.;
RT "IS231D, E and F, three new insertion sequences in Bacillus thuringiensis: extension of the IS231 family.";
RL Mol. Microbiol. 6:1959-1967(1992).
CC -!- FUNCTION: INVOLVED IN THE TRANSPOSITION OF THE INSERTION SEQUENCE.
CC -!- SIMILARITY: BELONGS TO THE TRANSPOSASE FAMILY 11.
CC -----
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CC -----
DR EMBL; X63384; CAA44990.1; -.
DR PIR; S25821; S25821.
DR InterPro; IPR002559; Transposase_11.
DR Pfam; PF01609; Transposase_11; 1.
KW Transposable element; Transposition; DNA-binding; DNA recombination.
SQ SEQUENCE 478 AA; 56087 MW; A0AAA4F46E61C223 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 478;
Best Local Similarity 83.3%; Pred.No. 71;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
||:|
Db 436 LIQLFH 441

RESULT 13
HEP2_HUMAN STANDARD; PRT; 499 AA.
AC P05546;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Heparin cofactor II precursor (HC-II) (Protease inhibitor leuserpin 2) (HLS2).
DN SERPIND1 OR HCF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91120782; PubMed-1671335;
RA Herzog R., Lutz S., Blin N., Marasa J.C., Blinder M.A., Tollefsen D.M.;
RT "Complete nucleotide sequence of the gene for human heparin cofactor II and mapping to chromosomal band 22q11.";
RL Biochemistry 30:1350-1357(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-88163663; PubMed-2894851;
RA Blinder M.A., Marasa J.C., Reynolds C.H., Deaven L.L., Tollefsen D.M.;
RT "Heparin cofactor II: cDNA sequence, chromosome localization, restriction fragment length polymorphism, and expression in Escherichia coli.";
RL Biochemistry 27:752-759(1988).
RN [3]

RP SEQUENCE OF 19-499 FROM N.A.
RX MEDLINE=86120356; PubMed=3003690;
RA Ragg H.;
RT "A new member of the plasma protease inhibitor gene family.";
RL Nucleic Acids Res. 14:1073-1088(1986).
RN [4]
RP SEQUENCE OF 333-499 FROM N.A.
RX MEDLINE=86242236; PubMed=3755044;
RA Inhorn R.C., Tollefsen D.M.;
RT "Isolation and characterization of a partial cDNA clone for heparin cofactor II.";
RT cofactor II.";
RL Biochem. Biophys. Res. Commun. 137:431-436(1986).
RN [5]
RP SEQUENCE OF 20-52 AND 464-499.
RX MEDLINE=86077723; PubMed=3907702;
RA Griffith M.J., Noyes C.M., Tyndall J.A., Church F.C.;
RT "Structural evidence for leucine at the reactive site of heparin cofactor II.";
RT Biochemistry 24:6777-6782(1985).
RN [6]
RP SEQUENCE OF 1-119 FROM N.A.
RX MEDLINE=88298901; PubMed=2841345;
RA Ragg H., Preibisch G.;
RT "Structure and expression of the gene coding for the human serpin hLS2.";
RL J. Biol. Chem. 263:12129-12134(1988).
RN [7]
RP SEQUENCE OF 58-85.
RX MEDLINE=91093260; PubMed=1985958;
RA Church F.C., Pratt C.W., Hoffman M.;
RT "Leukocyte chemoattractant peptides from the serpin heparin cofactor II.";
RL J. Biol. Chem. 266:704-709(1991).
RN [8]
RP FUNCTION OF N-TERMINAL ACIDIC DOMAIN.
RX MEDLINE=92041850; PubMed=1939083;
RA van Deerlin V.M.D., Tollefsen D.M.;
RT "The N-terminal acidic domain of heparin cofactor II mediates the inhibition of alpha-thrombin in the presence of glycosaminoglycans.";
RL J. Biol. Chem. 266:20223-20231(1991).
RN [9]
RP MUTAGENESIS OF ARG-122 AND LYS-204.
RX MEDLINE=90094412; PubMed=2104620;
RA Blinder M.A., Tollefsen D.M.;
RT "Site-directed mutagenesis of arginine 103 and lysine 185 in the proposed glycosaminoglycan-binding site of heparin cofactor II.";
RL J. Biol. Chem. 265:286-291(1990).
RN [10]
RP VARIANT OSLO HIS-208.
RX MEDLINE=89174798; PubMed=2647747;
RA Blinder M.A., Andersson T.R., Abildgaard U., Tollefsen D.M.;
RT "Heparin cofactor II Oslo. Mutation of Arg-189 to His decreases the affinity for dermatan sulfate.";
RL J. Biol. Chem. 264:5128-5133(1989).
RN [11]
RP VARIANTS THR-7; HIS-208 AND MET-442.
RX MEDLINE=99318093; PubMed=10391209;
RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q., Lander E.S.;
RT "Characterization of single-nucleotide polymorphisms in coding regions of human genes.";
RL Nat. Genet. 22:231-238(1999).
RN [12]
RP ERRATUM.
RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q., Lander E.S.;
RL Nat. Genet. 23:373-373(1999).
CC -1- FUNCTION: THROMBIN INHIBITOR ACTIVATED BY THE GLYCOSAMINOGLYCANS, HEPARIN OR DERMATAN SULFATE. IN THE PRESENCE OF THE LATTER,

CC HC-II BECOMES THE PREDOMINANT THROMBIN INHIBITOR IN PLACE OF
CC ANTITHROMBIN III (AT). ALSO INHIBITS CHYMOTRYPSIN, BUT IN A
CC GLYCOSAMINOGLYCAN-INDEPENDENT MANNER.
CC -1- FUNCTION: PEPTIDES AT THE N-TERMINAL OF HC-II HAVE CHEMOTACTIC
CC ACTIVITY FOR BOTH MONOCYTES AND NEUTROPHILS.
CC -1- TISSUE SPECIFICITY: Expressed predominantly in liver.
CC -1- DOMAIN: THE N-TERMINAL ACIDIC REPEAT REGION MEDIATES, IN PART, THE
CC GLYCOSAMINOGLYCAN-ACCELERATED THROMBIN INHIBITION.
CC -1- DISEASE: DEFECTS IN SERPIND1 ARE ASSOCIATED WITH THROMBOSIS
CC (THROMBOPHILIA).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC -----
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CC -----
CC EMBL; M58600; AAS52641.1; -
DR EMBL; X03498; CAA27218.1; ALT_INIT.
DR EMBL; M12849; AAS52642.1; -
DR EMBL; M33660; AAS36185.1; -
DR PIR; A37924; A37924.
DR PDB; 1JMJ; 30-AUG-02.
DR PDB; 1JMO; 30-AUG-02.
DR Genew; HGNC:4838; SERPIND1.
DR MIM; 142360; -
DR InterPro; IPR000295; Leuserpin2.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR PRINTS; PR00780; LEUSERPINII.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin; Serine protease inhibitor; Glycoprotein; Heparin-binding;
KW Plasma; Blood coagulation; Chemotaxis; Signal; Thrombophilia;
KW Disease mutation; Sulfation; Repeat; Polymorphism; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 499 HEPARIN COFACTOR II.
FT DOMAIN 68 79 CHEMOTACTIC ACTIVITY.
FT DOMAIN 73 97 2 X 11 AA APPROXIMATE REPEATS, ASP/GLU-
FT REPEAT 73 83 RICH (ACIDIC) (HIRUDIN-LIKE).
FT REPEAT 87 97 1.
FT DOMAIN 192 212 2. GLYCOSAMINOGLYCAN-BINDING SITE.
FT MOD_RES 79 79 SULFATION.
FT MOD_RES 92 92 SULFATION.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT ACT_SITE 463 464 REACTIVE BOND (BY SIMILARITY).
FT VARIANT 7 7 A -> T (IN dbSNP:5905).
FT VARIANT 60 60 /FTid=VAR_011746.
FT VARIANT 60 60 H -> P (IN dbSNP:165867).
FT VARIANT 208 208 /FTid=VAR_011747.
FT VARIANT 208 208 R -> H (IN OSLO; HCF2 DEFICIENCY;
FT DECREASED AFFINITY FOR DERMATAN SULFATE;
FT dbSNP:6065).
FT VARIANT 237 237 /FTid=VAR_007112.
FT VARIANT 442 442 K -> R (IN dbSNP:1042435).
FT MUTAGEN 122 122 T -> M (IN dbSNP:5904).
FT MUTAGEN 122 122 /FTid=VAR_011749.
FT MUTAGEN 122 122 R -> L: NORMAL THROMBIN INHIBITION AND
FT MUTAGEN 122 122 GLYCOSAMINOGLYCAN AFFINITY.
FT MUTAGEN 122 122 R -> Q: GREATLY REDUCED THROMBIN
FT MUTAGEN 122 122 INHIBITION. NORMAL GLYCOSAMINOGLYCAN
FT MUTAGEN 122 122 AFFINITY.
FT MUTAGEN 122 122 R -> W: GREATLY REDUCED THROMBIN
FT MUTAGEN 204 204 INHIBITION. NORMAL GLYCOSAMINOGLYCAN
FT MUTAGEN 204 204 AFFINITY.
FT MUTAGEN 204 204 K -> M: REDUCED HEPARIN- AND NO DERMATAN

FT MUTAGEN 204 204 SULFATE-ACTIVATED INHIBITION.
FT K->N: REDUCED HEPARIN- AND NO DERMATAN
FT SULFATE-ACTIVATED INHIBITION.
FT K->I: REDUCED HEPARIN- AND NO DERMATAN
FT SULFATE-ACTIVATED INHIBITION.
FT MISSING (IN REF. 5).
FT CONFLICT 49 49 R -> P (IN REF. 5).
FT CONFLICT 483 483 C -> T (IN REF. 5).
FT CONFLICT 486 486 S -> Q (IN REF. 5).
FT CONFLICT 499 499
SQ SEQUENCE 499 AA: 57070 MW: 3BC0E353FE1F6DF05 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 499;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
: : : : :
Db 113 LIQLFH 118

RESULT 14
YNA8_YEAST STANDARD; PRT; 569 AA.
ID YNA8_YEAST
AC P53983;
DT 01-OCT-1996 (Rel. 34, Created)
DI 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hypothetical 76.7 kDa protein in SPO1-SIS1 intergenic region.
GN YNL008C OR N2874.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE OF 1-102 FROM N.A.
RA Andre B., Iraqui Houssaini I., Urrestarazu L.A., Vissers S.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DDHJ databases.
RN [2]
RP SEQUENCE OF 371-669 FROM N.A.
RA Daignon F., Crouzet M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----
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CC -----
DR EMBL: 271284; CAA95868.1; -;
DR EMBL: 271283; CAA95867.1; -;
DR PIR: S62919; S62919.
DR SGD: S0004953; ASI3.
DR GO: GO:0005789; C: endoplasmic reticulum membrane; IGI.
DR GO: GO:0004842; F: ubiquitin-protein ligase activity; IGI.
DR GO: GO:0006511; P: ubiquitin-dependent protein catabolism; IGI.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 72 92 POTENTIAL.
FT TRANSMEM 120 140 POTENTIAL.
FT TRANSMEM 150 170 POTENTIAL.
FT TRANSMEM 175 195 POTENTIAL.
FT TRANSMEM 209 229 POTENTIAL.
FT TRANSMEM 234 254 POTENTIAL.
FT TRANSMEM 271 291 POTENTIAL.
SQ SEQUENCE 669 AA: 76741 MW: 1BB4DCAC74E8FF63 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 669;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6

Db 223 LVLEFH 228
: : : : :

RESULT 15
CLC6_HUMAN STANDARD; PRT; 869 AA.
ID CLC6_HUMAN
AC P51797; O60818; O60819; O60820; O60821; P78520; P78521; Q99427;
AC Q99428; Q99429;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Chloride channel protein 6 (CLC-6).
GN CLCN6 OR KIAA0046.
CS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RX MEDLINE=96130311; PubMed=8543009;
RA Brandt S., Jentsch T.J.;
RT "CLC-6 and CLC-7 are two novel broadly expressed members of the CLC
RT chloride channel family.";
RL FEBS Lett. 377:15-20(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D), AND SEQUENCE OF 1-409 FROM
RP N.A. (ISOFORM A).
RX TISSUE=Chronic myeloid leukemia cell;
RX MEDLINE=97344267; PubMed=9224655;
RA Eggermont J., Buyse G., Voets T., Tytgat J., De Smedt H.,
RA Droogmans G., Nilius B.;
RT "Alternative splicing of CLC-6 (a member of the CLC chloride-channel
RT family) transcripts generates three truncated isoforms one of which,
RT CLC-6c, is kidney-specific.";
RL Biochem. J. 325:269-276(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=99431565; PubMed=10500249;
RA Kornak U., Boesl M.R., Kubisch C.;
RT "Complete genomic structure of the CLCN6 and CLCN7 putative chloride
RT channel genes.";
RL Biochim. Biophys. Acta 1447:100-106(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RA Ohara O., Nagase T., Kikuno R., Nomura N.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE OF 50-869 FROM N.A., AND ALTERNATIVE SPLICING.
RA Errington H.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE OF 237-869 FROM N.A. (ISOFORM A).
RC TISSUE=Bone marrow;
RX MEDLINE=96051398; PubMed=7584044;
RA Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,
RA Seki N., Kawarabayashi Y., Ishikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. II.
RT The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced by
RT analysis of cDNA clones from human cell line KG-1.";
RL DNA Res. 1:223-229(1994).
RN [7]
RP TISSUE SPECIFICITY.
RC TISSUE=Aortic endothelium, and Vascular smooth muscle;
RX MEDLINE=99222497; PubMed=10198195;
RA Lamb F.S., Clayton G.H., Liu B.-X., Smith R.L., Barna T.J.,
RA Schutte B.C.;
RT "Expression of CLCN voltage-gated chloride channel genes in human
RT blood vessels.";
RL J. Mol. Cell. Cardiol. 31:657-666(1999).
CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE

CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC TRANSEPITHELIAL TRANSPORT.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=4;
CC Name=A; Synonyms=CLC-6a;
CC IsoId=P51797-1; Sequence=Displayed;
CC Name=B; Synonyms=CLC-6b, D2-A1;
CC IsoId=P51797-2; Sequence=VSP_001043, VSP_001044;
CC Name=C; Synonyms=CLC-6c, D1-A1;
CC IsoId=P51797-3; Sequence=VSP_001045, VSP_001046;
CC Name=D; Synonyms=CLC-6d, D1-A2;
CC IsoId=P51797-4; Sequence=VSP_001047, VSP_001048;
CC -|- TISSUE SPECIFICITY: Testis, ovary, small intestine, brain and
CC skeletal muscle. Low level expression in aortic and coronary
CC vascular smooth muscle cells, and aortic endothelial cells.
CC Isoform C is only detected in kidney.
CC -|- SIMILARITY: Belongs to the chloride channel family.
CC -|- SIMILARITY: Contains 2 CBS domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X83378; CAA58292.1; -;
DR EMBL; X96391; CAA65255.1; -;
DR EMBL; X99472; CAA67835.1; -;
DR EMBL; X99473; CAA67836.1; -;
DR EMBL; X99474; CAA67837.1; -;
DR EMBL; X99475; CAA67838.1; -;
DR EMBL; AF009257; AAB69287.1; -;
DR EMBL; AF009247; AAB69287.1; JOINED.
DR EMBL; AF009248; AAB69287.1; JOINED.
DR EMBL; AF009249; AAB69287.1; JOINED.
DR EMBL; AF009250; AAB69287.1; JOINED.
DR EMBL; AF009251; AAB69287.1; JOINED.
DR EMBL; AF009252; AAB69287.1; JOINED.
DR EMBL; AF009253; AAB69287.1; JOINED.
DR EMBL; AF009254; AAB69287.1; JOINED.
DR EMBL; AF009255; AAB69287.1; JOINED.
DR EMBL; AF009256; AAB69287.1; JOINED.
DR EMBL; AL021155; CAA15951.1; -;
DR EMBL; AL021155; CAA15952.1; -;
DR EMBL; AL021155; CAA15953.1; -;
DR EMBL; AL021155; CAA15954.1; -;
DR EMBL; D28475; BAA05836.3; -;
DR Genew; HGNC:2024; CLCN6.
DR MIM; 602726; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005247; F:voltage-gated chloride channel activity; NAS.
DR GO; GO:0006821; P:chloride transport; NAS.
DR GO; GO:0006884; P:regulation of cell volume; NAS.
DR GO; GO:0007165; P:signal transduction; NAS.
DR GO; GO:0006832; P:small molecule transport; TAS.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR001807; Cl-channel_volt.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00654; voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
KW Ionic channel; Ion transport; Chloride channel; Chloride;
KW Voltage-gated channel; Transmembrane; CBS domain; Repeat;
KW Alternative splicing.
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 130 150 POTENTIAL.
FT TRANSMEM 184 204 POTENTIAL.
FT TRANSMEM 245 265 POTENTIAL.
FT TRANSMEM 334 354 POTENTIAL.
FT TRANSMEM 375 395 POTENTIAL.

FT TRANSMEM 462 482 POTENTIAL.
FT TRANSMEM 511 531 POTENTIAL.
FT DOMAIN 603 658 CBS 1.
FT DOMAIN 805 856 CBS 2.
FT DOMAIN 4 18 CYS-RICH.
FT VARSPLIC 237 320 DKRDFVSAGAAAGVAAAFCAPIGGTFLFSLEEGSFNNQGLT
WKVLFCSMSATFTLNFFRSIGIQFGSWGSQLPGLNFGFEK
CS -> YGKRQERLCISRSGCWSCCFCRGANRGYLVQSRGG
FVLEPRAHVESALLFHVCHLHPQLLPFFWDSVWKLGLPAP
WIAELWRV (in isoform B).
/FTId-VSP_001043.
Missing (in isoform B).
/FTId-VSP_001044.
CSDSKKCHLWTAMDGLGFFVVMGVIGLLGATFNC -> SL
REPCVSGNHRGGVCGLDGVRMPDVLFSNR (in
isoform C).
/FTId-VSP_001045.
Missing (in isoform C).
/FTId-VSP_001046.
DKRDFVSAGAAAGVAAAFCAPIGGTFLFSLEEGSFNNQGLT
WKVLFCSMSATFTLNFFRSIGIQFGSWGSQL -> SGCWSC
CSRGANRGYLVQSRGGFVLEPRAHVESALLFHVCHLHPQ
LLPFDWSVWKLGLPAPWIAELWRV (in isoform D).
/FTId-VSP_001047.
Missing (in isoform D).
/FTId-VSP_001048.
G -> E (IN REF. 5).
SQ SEQUENCE 869 AA; 97216 MW; E4273777D9FF4328 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 869;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
:|||||
Db 450 ILQLFH 455

Search completed: October 14, 2003, 14:34:03
Job time : 6.41667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 ; Search time 19.875 Seconds
(without alignments)
77.903 Million cell updates/sec

Title: US-09-881-490-150
Perfect score: 31
Sequence: 1 LIQLFH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archcap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 31 | 100.0 | 146 | 16 Q9CHG1 | Q9chgl lactococcus |
| 2 | 31 | 100.0 | 487 | 4 Q81W58 | Q81w58 homo sapien |
| 3 | 31 | 100.0 | 898 | 16 Q8DP20 | Q8dp20 streptococc |
| 4 | 31 | 100.0 | 914 | 16 Q97PQ2 | Q97pq2 streptococc |
| 5 | 30 | 96.8 | 1039 | 2 P72534 | P72534 streptococc |
| 6 | 30 | 96.8 | 3152 | 12 Q8UZ37 | Q8uz37 leek yellow |
| 7 | 29 | 93.5 | 136 | 11 Q8B2C2 | Q8bzc2 mus musculu |
| 8 | 29 | 93.5 | 312 | 11 Q9JIN8 | Q9jin8 mus musculu |
| 9 | 29 | 93.5 | 312 | 11 Q9DCE2 | Q9dce2 mus musculu |
| 10 | 29 | 93.5 | 312 | 11 Q8R3P0 | Q8r3p0 mus musculu |
| 11 | 29 | 93.5 | 312 | 11 Q9D876 | Q9d876 mus musculu |
| 12 | 29 | 93.5 | 314 | 11 Q9R1T5 | Q9rlt5 rattus norv |
| 13 | 29 | 93.5 | 379 | 5 Q9VX89 | Q9vx89 drosophila |
| 14 | 29 | 93.5 | 1627 | 10 Q8LQJ0 | Q8lqj0 oryza sativ |
| 15 | 28 | 90.3 | 179 | 16 Q9KQH7 | Q9kqh7 bacillus ha |
| 16 | 28 | 90.3 | 212 | 3 Q92334 | Q92334 sphaceloma |

| | | | | | |
|----|----|------|------|-----------|--------------------|
| 17 | 28 | 90.3 | 261 | 2 Q9AOB6 | Q9aqb6 actinobacil |
| 18 | 28 | 90.3 | 288 | 5 Q8IAB2 | Q8iab2 caenorhabdi |
| 19 | 28 | 90.3 | 351 | 16 Q8RGG6 | Q8rgg6 fusobacteri |
| 20 | 28 | 90.3 | 469 | 4 Q9NPT5 | Q9npt5 homo sapien |
| 21 | 28 | 90.3 | 659 | 4 Q43764 | Q43764 homo sapien |
| 22 | 28 | 90.3 | 697 | 4 Q9NXJ9 | Q9nxj9 homo sapien |
| 23 | 28 | 90.3 | 703 | 11 Q91YI9 | Q91yi9 mus musculu |
| 24 | 28 | 90.3 | 706 | 4 Q8NB85 | Q8nb85 homo sapien |
| 25 | 28 | 90.3 | 711 | 5 Q18098 | Q18098 caenorhabdi |
| 26 | 28 | 90.3 | 717 | 4 Q8IUN6 | Q8iun6 homo sapien |
| 27 | 28 | 90.3 | 721 | 4 Q96KL1 | Q96kl1 homo sapien |
| 28 | 28 | 90.3 | 721 | 11 Q9QWV2 | Q9qvw2 mus musculu |
| 29 | 28 | 90.3 | 723 | 4 Q8NIB4 | Q8nlb4 homo sapien |
| 30 | 28 | 90.3 | 723 | 11 Q55166 | Q55166 rattus norv |
| 31 | 28 | 90.3 | 723 | 11 Q8C754 | Q8c754 mus musculu |
| 32 | 28 | 90.3 | 723 | 11 Q8BQ15 | Q8bql5 mus musculu |
| 33 | 28 | 90.3 | 833 | 11 Q923L0 | Q923l0 mus musculu |
| 34 | 28 | 90.3 | 1095 | 4 Q9HCG6 | Q9hcg6 homo sapien |
| 35 | 28 | 90.3 | 1904 | 13 Q8AV28 | Q8av28 gallus gall |
| 36 | 28 | 90.3 | 2003 | 11 Q91Y51 | Q91y51 mus musculu |
| 37 | 28 | 90.3 | 2024 | 4 Q15154 | Q15154 homo sapien |
| 38 | 28 | 90.3 | 2025 | 11 Q9R0L6 | Q9r0l6 mus musculu |
| 39 | 28 | 90.3 | 2031 | 13 Q9PVV4 | Q9pvv4 xenopus lae |
| 40 | 28 | 90.3 | 2075 | 13 Q90WA4 | Q90wa4 fugu rubrip |
| 41 | 28 | 90.3 | 2075 | 13 Q8JG44 | Q8jg44 fugu rubrip |
| 42 | 28 | 90.3 | 2301 | 10 Q80784 | Q80784 arabidopsis |
| 43 | 27 | 87.1 | 24 | 5 Q94371 | Q94371 caenorhabdi |
| 44 | 27 | 87.1 | 110 | 11 Q8VDG9 | Q8vdbg mus musculu |
| 45 | 27 | 87.1 | 143 | 2 Q925V2 | Q9z5v2 bacillus th |

ALIGNMENTS

RESULT 1

Q9CHG1
ID Q9CHG1 PRELIMINARY; PRT; 146 AA.
AC Q9CHG1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Transcriptional regulator.
GN RMAG OR LL0770.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT *The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403.*;
RL Genome Res. 11:731-753(2001).
CC -1- SIMILARITY: BELONGS TO THE MARR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; AB006310; AAK04868.1; -.
DR InterPro; IPR000835; HTH_Marr.
DR Pfam; PF01047; Marr; 1.
DR PRINTS; PR00598; HTHMARR.
DR SMART; SM00347; HTH_MARR; 1.
KW DNA-binding; Transcription regulation; Complete proteome.
SQ SEQUENCE 146 AA; 16808 MW; 30CF04E38EB45953 CRC64;

Query Match 100.0%; Score 31; DB 16; Length 146;
Best Local Similarity 100.0%; Pred. NO. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIQLFH 6

Db 12 LIQLFH 17

RESULT 2

Q8IW58 PRELIMINARY; PRT; 487 AA.
AC Q8IW58;
DI 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DI 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to bactericidal/permeability-increasing protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040955; AAH40955.1; -.
SQ SEQUENCE 487 AA; 53880 MW; FE709D9317E5206D CRC64;

Query Match 100.0%; Score 31; DB 4; Length 487;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIQLFH 6
|:||||
Db 185 LIQLFH 190

RESULT 3

Q8DP20 PRELIMINARY; PRT; 898 AA.
AC Q8DP20;
DI 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DI 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P-type ATPase-calcium transporter (EC 3.6.1.36).
GN PACL OR SPRI410.
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=171101;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21429245; PubMed=11544234;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczyk L.C., Burgett S.,
RA DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostock P.R. Jr., Skatrud P.L.,
RA Glass J.L.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL J. Bacteriol. 183:5709-5717(2001).
DR EMBL; AE008510; AAL00214.1; -.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 898 AA; 97039 MW; A7AF2CDFBFBF9E6D4 CRC64;

Query Match 100.0%; Score 31; DB 16; Length 898;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIQLFH 6
|:||||
Db 806 LIQLFH 811

RESULT 4

Q97PQ2 PRELIMINARY; PRT; 914 AA.
ID Q97PQ2

O97PQ2;
AC 01-OCT-2001 (TrEMBLrel. 18, Created)
DI 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DI 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cation-transporting ATPase, E1-E2 family.
GN SP1551.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";
RL Science 293:498-506(2001).
DR EMBL; AE007449; AAK75638.1; -.
DR TIGR; SP1551; -.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR006068; Cation_ATPase_C.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Hydrolase.
DR InterPro; IPR000695; H_ATPase.
DR Pfam; PF00689; Cation_ATPase_C; 1.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR PRINTS; PR00120; HATPASE.
DR TIGRFAMS; TIGR01494; ATPase_P-type; 6.
DR PROSITE; PS00154; ATPASE_E1_E2; 1.
DR Complete proteome.
KW SEQUENCE 914 AA; 99051 MW; C86323039FE51850 CRC64;
SQ

Query Match 100.0%; Score 31; DB 16; Length 914;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIQLFH 6
|:||||
Db 822 LIQLFH 827

RESULT 5

P72534 PRELIMINARY; PRT; 1039 AA.
ID P72534;
AC P72534;
DI 01-FEB-1997 (TrEMBLrel. 02, Created)
DI 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Protein F2.
GN PRTF2.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=100076;
RX MEDLINE=97011581; PubMed=8858591;
RA Jaffe J., Natanson-Yaron S., Caparon M.G., Hanski E.;
RT "Protein F2, a novel fibronectin-binding protein from Streptococcus pyogenes, possesses two binding domains.";
RL Mol. Microbiol. 21:373-384(1996).

DR EMBL: U31980; AAC44522.1; -.
DR InterPro: IPR004237; Fn_bind.
DR Pfam: PF02986; Fn_bind; 4.
SQ SEQUENCE 1039 AA; 115037 MW; DEC806A1B1A2FC3A CRC64;

Query Match 96.8%; Score 30; DB 2; Length 1039;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
|:||||
Db 972 LVQLFH 977

RESULT 6
Q8UZ37 PRELIMINARY; PRT; 3152 AA.
AC Q8UZ37;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE polyprotein.
OS leek yellow stripe potyvirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Polyviridae;
OC Potyvirus.
OX NCBI_TaxID=42004;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Yuhang GYH; PubMed=11890533;
RX MEDLINE=21887390; PubMed=11890533;
RA Chen J., Chen J.P., Adams M.J.;
RT "Characterisation of some carla- and potyviruses from bulb crops in
RT China.";
RL Arch. Virol. 147:419-428(2002).
CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
DR EMBL: AJ307057; CAC85226.1; -.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR001730; Peptidase_C4.
DR InterPro: IPR001456; Peptidase_C6.
DR InterPro: IPR001592; Poty_coat.
DR InterPro: IPR002540; Poty_P1.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR007094; RNA_pol_PSwir.
DR Pfam: PF00271; helicase_C; 1.
DR Pfam: PF00863; Peptidase_C4; 1.
DR Pfam: PF00851; Peptidase_C6; 1.
DR Pfam: PF00767; Poty_coat; 1.
DR Pfam: PF01577; Poty_P1; 1.
DR Pfam: PF00680; RNA_dcp_RNA_pol; 1.
DR PRINTS: PR00966; NIAPOTYPTASE.
DR SMART: SM00487; DEXDc; 1.
DR SMART: SM00490; HELICc; 1.
DR PROSITE: PS50507; RDRP_POSITIVE; 1.
DR PROSITE: PS50521; RDRP_VIRAL; 1.
KW ATP-binding; Coat protein; Helicase; Hydrolase.
FT CHAIN 1 362
FT CHAIN 363 818
FT CHAIN 819 1177
FT CHAIN 1178 1229
FT CHAIN 1230 1864
FT CHAIN 1865 1917
FT CHAIN 1918 2109
FT CHAIN 2110 2351
FT CHAIN 2352 2864
FT CHAIN 2865 3152
SQ SEQUENCE 3152 AA; 357600 MW; EB881A928A5FA16D CRC64;

Query Match 96.8%; Score 30; DB 12; Length 3152;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
|:||||
Db 403 LVQLFH 408

RESULT 7
Q8BZC2 PRELIMINARY; PRT; 136 AA.
AC Q8BZC2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Aspartoacylase (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL: AK035910; BAC29240.1; -.
FT NON_TER 1
SQ SEQUENCE 136 AA; 15735 MW; 05B4CC681FEAB785 CRC64;

Query Match 93.5%; Score 29; DB 11; Length 136;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
|:||||
Db 85 LIQMFH 90

RESULT 8
Q9JIN8 PRELIMINARY; PRT; 312 AA.
AC Q9JIN8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Aspartoacylase ASPA.
GN ASPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20299153; PubMed=10837925;
RA Namboudiri M.A., Corigliano-Murphy A., Jiang G., Rollag M.,
RA Provencio I.;
RT "Murine aspartoacylase: cloning, expression and comparison with the
RT human enzyme.";
RL Brain Res. Mol. Brain Res. 77:285-289(2000).
DR EMBL: AF212998; AAF76459.1; -.
DR MGD: MGI:87914; Aspa.
DR InterPro: IPR007036; Aste_Aspa.
DR Pfam: PF04952; Aste_Aspa; 1.
SQ SEQUENCE 312 AA; 35304 MW; 65A8C55F20F1755B CRC64;

Query Match 93.5%; Score 29; DB 11; Length 312;
Best Local Similarity 83.3%; Pred. No. 93;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
|:||||
Db 135 LIQMFH 140

```

DR InterPro: IPR007036; Aste_Aspa.
DR Pfam: PF04952; Aste_Aspa; 1.
SQ SEQUENCE 312 AA; 35344 MW; 7328C55F20FI755B CRC64;

Query Match          93.5%; Score 29; DB 11; Length 312;
Best Local Similarity 83.3%; Pred. NO. 93;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 135 LIQMFH 140

RESULT 11
Q9D876 PRELIMINARY; PRT; 312 AA.
AC Q9D876;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Aspartoacylase (Aminoacylase) 2.
GN ASPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RI "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK002859; BAB22412.1; -.
DR MGD; MGI:87914; Aspa.
DR InterPro; IPR007036; Aste_Aspa.
DR Pfam; PF04952; Aste_Aspa; 1.
SQ SEQUENCE 312 AA; 35344 MW; F09E710CC3107108 CRC64;

Query Match          93.5%; Score 29; DB 11; Length 312;
Best Local Similarity 83.3%; Pred. NO. 93;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 135 LIQMFH 140

RESULT 10
Q8R3P0 PRELIMINARY; PRT; 312 AA.
AC Q8R3P0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Aspartoacylase (Aminoacylase) 2.
GN ASPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DOBJ databases.
DR EMBL; BC024934; AAH24934.1; -.
DR MGD; MGI:87914; Aspa.
```

GN ASPA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WTC; TISSUE=Brain;
RA Kitada K., Serikawa T.;
RT *Full length rat cDNA coding for aspartoacylase.*;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB023432; BAA82801.1; -;
DR InterPro; IPR007036; Aste_ASPA.
DR Pfam; PF04952; Aste_ASPA; 1.
SQ SEQUENCE 314 AA; 35580 MW; 6F307333F7334F86 CRC64;

Query Match 93.5%; Score 29; DB 11; Length 314;
Best Local Similarity 83.3%; Pred. NO. 93;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 135 LIQMFH 140
|||:|

RESULT 13
Q9VX89
ID Q9VX89 PRELIMINARY; PRT; 379 AA.
AC Q9VX89;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE CG12433 protein.
GN CG12433.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazei R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baliew R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
RA Beeson K.Y., Bencs P.V., Berman B.P., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Konnison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT *The genome sequence of Drosophila melanogaster.*;
RL Science 287:2185-2195(2000).
DR EMBL; AE003504; AAF48689.1; -;
DR FlyBase; FBgn0030811; CG12433.
SQ SEQUENCE 379 AA; 43974 MW; 8F24898E3F489A13 CRC64;

Query Match 93.5%; Score 29; DB 5; Length 379;
Best Local Similarity 83.3%; Pred. NO. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 195 LLQLFH 200
|||:|

RESULT 14
Q8LQJ0
ID Q8LQJ0 PRELIMINARY; PRT; 1627 AA.
AC Q8LQJ0;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE P0456E05.12 protein.
GN P0456E05.12.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT *Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0456E05.*;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003416; BAB92613.1; -;
DR Gramene; Q8LQJ0; -;
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR005034; DUF283.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR003100; PAZ.
DR InterPro; IPR000999; RNase_3.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF03368; DUF283; 1.
DR Pfam; PF00271; helicase_C; 1.
DR Pfam; PF02170; PAZ; 1.
DR Pfam; PF00636; Ribonuclease_3; 1.
DR Pfam; PF00096; zf-C2H2; 1.
DR SMART; SM00490; HELICC; 1.
DR SMART; SM00535; RIBOC; 2.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS50821; PAZ; 1.
DR PROSITE; PS00517; RNASE_3_1; 1.
DR PROSITE; PS50142; RNASE_3_2; 2.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW ATP-binding; Helicase; Hydrolase; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 1627 AA; 180368 MW; DF7776452C2068F0 CRC64;

Query Match 93.5%; Score 29; DB 10; Length 1627;
Best Local Similarity 83.3%; Pred. NO. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
Db 195 LLQLFH 200
|||:|

Db 226 LIQIFH 231

RESULT 15

Q9KGH7 PRELIMINARY; PRT; 179 AA.
AC Q9KGH7;
DT 01-OCT-2000 (TREMHLrel. 15, Created)
DT 01-OCT-2000 (TREMHLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMHLrel. 23, Last annotation update)
DE Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8).
GN HPRT OR BH0084.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT *Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.*;
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; AP001507; BAB03803.1; -.
DR HSSP; P51900; 1HCX.
DR InterPro; IPR005904; Hxn_phspho_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; PRtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMS; TIGR01203; HGPRTase; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW Glycosyltransferase; Transferase; Complete proteome.
SQ SEQUENCE 179 AA; 20139 MW; BA0B681C58D83BC9 CRC64;

Query Match 90.3%; Score 28; DB 16; Length 179;
Best Local Similarity 83.3%; Pred. No. 94;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIQLFH 6
//:||||
Db 110 LIQLFH 115

Search completed: October 14, 2003, 14:36:50
Job time : 22.875 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:19 ; Search time 25.75 Seconds
(without alignments)
36.985 Million cell updates/sec

Title: US-09-881-490-154
Perfect score: 33
Sequence: 1 WLQLK 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | length | DB ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 33 | 100.0 | 6 | 17 AAW04065 | Antifungal peptid |
| 2 | 33 | 100.0 | 6 | 18 AAW44553 | Anti-fungal peptid |
| 3 | 33 | 100.0 | 6 | 18 AAW43743 | Bactericidal/perme |
| 4 | 33 | 100.0 | 6 | 20 AAY00530 | Antifungal peptid |
| 5 | 33 | 100.0 | 6 | 22 AAB65454 | Anti-fungal peptid |
| 6 | 33 | 100.0 | 7 | 17 AAW04025 | Antifungal peptid |
| 7 | 33 | 100.0 | 7 | 17 AAW04026 | Antifungal peptid |
| 8 | 33 | 100.0 | 7 | 18 AAW44554 | Anti-fungal peptid |
| 9 | 33 | 100.0 | 7 | 18 AAW44555 | Anti-fungal peptid |

| | | | | | |
|----|----|-------|---|-------------|--------------------|
| 10 | 33 | 100.0 | 7 | 18 AAW43746 | Bactericidal/perme |
| 11 | 33 | 100.0 | 7 | 18 AAW43744 | Bactericidal/perme |
| 12 | 33 | 100.0 | 7 | 18 AAW43745 | Bactericidal/perme |
| 13 | 33 | 100.0 | 7 | 20 AAY00531 | Antifungal peptid |
| 14 | 33 | 100.0 | 7 | 20 AAY00532 | Antifungal peptid |
| 15 | 33 | 100.0 | 7 | 22 AAB65455 | Anti-fungal peptid |
| 16 | 33 | 100.0 | 7 | 22 AAB65456 | Anti-fungal peptid |
| 17 | 33 | 100.0 | 8 | 17 AAW04027 | Antifungal peptid |
| 18 | 33 | 100.0 | 8 | 17 AAW04029 | Antifungal peptid |
| 19 | 33 | 100.0 | 8 | 18 AAW44556 | Anti-fungal peptid |
| 20 | 33 | 100.0 | 8 | 18 AAW44558 | Anti-fungal peptid |
| 21 | 33 | 100.0 | 8 | 18 AAW43748 | Bactericidal/perme |
| 22 | 33 | 100.0 | 8 | 20 AAY00535 | Antifungal peptid |
| 23 | 33 | 100.0 | 8 | 20 AAY00533 | Antifungal peptid |
| 24 | 33 | 100.0 | 8 | 22 AAB65457 | Anti-fungal peptid |
| 25 | 33 | 100.0 | 8 | 22 AAB65459 | Anti-fungal peptid |
| 26 | 33 | 100.0 | 9 | 17 AAW04030 | Antifungal peptid |
| 27 | 33 | 100.0 | 9 | 17 AAW04031 | Antifungal peptid |
| 28 | 33 | 100.0 | 9 | 18 AAW44559 | Antifungal peptid |
| 29 | 33 | 100.0 | 9 | 18 AAW44561 | Anti-fungal peptid |
| 30 | 33 | 100.0 | 9 | 18 AAW44563 | Anti-fungal peptid |
| 31 | 33 | 100.0 | 9 | 18 AAW44564 | Anti-fungal peptid |
| 32 | 33 | 100.0 | 9 | 18 AAW44565 | Anti-fungal peptid |
| 33 | 33 | 100.0 | 9 | 18 AAW44572 | Anti-fungal peptid |
| 34 | 33 | 100.0 | 9 | 18 AAW43754 | Bactericidal/perme |
| 35 | 33 | 100.0 | 9 | 18 AAW43753 | Bactericidal/perme |
| 36 | 33 | 100.0 | 9 | 18 AAW43749 | Bactericidal/perme |
| 37 | 33 | 100.0 | 9 | 20 AAY00536 | Antifungal peptid |
| 38 | 33 | 100.0 | 9 | 20 AAY00538 | Antifungal peptid |
| 39 | 33 | 100.0 | 9 | 20 AAY00540 | Antifungal peptid |
| 40 | 33 | 100.0 | 9 | 20 AAY00541 | Antifungal peptid |
| 41 | 33 | 100.0 | 9 | 20 AAY00542 | Antifungal peptid |
| 42 | 33 | 100.0 | 9 | 20 AAY00549 | Antifungal peptid |
| 43 | 33 | 100.0 | 9 | 21 AAY88384 | Antifungal peptid |
| 44 | 33 | 100.0 | 9 | 22 AAB65460 | Anti-fungal peptid |
| 45 | 33 | 100.0 | 9 | 22 AAB65462 | Anti-fungal peptid |

ALIGNMENTS

RESULT 1
AAW04065
ID AAW04065 standard; peptid; 6 AA.

XX AAW04065;
AC AAW04065;
XX 04-NOV-1996 (first entry)
XX Antifungal peptid XMP.321.
DE Antifungal peptid XMP.321.
XX Antifungal peptid; inhibitor; Domain Iii; polymorphonuclear leukocyte;
KW bactericidal/permeability-increasing protein; BPI; mammalian; PMN; fungi;
KW neutrophil; replication inhibitor; fungal infection; Aspergillus;
KW Cryptococcus; Candida; C.albicans; C.galabrat; C.krusei; C.lusitaniae;
KW C.parapsilosis; C.tropicalis; therapy.
XX Synthetic.
XX
FH Key Location/Qualifiers
ET Modified-site 6 /note= "amidated"
ET XX
XX
PN WO9508509-A1.
XX
PD 21-MAR-1996.
XX
PF 20-JUL-1995; 95WO-US09262.
XX
PR 13-JAN-1995; 95US-0372105.
PR 15-SEP-1994; 94US-0306473.
XX
PA (XOMA) XOMA CORP.

XX Fadem MB, Lim E, Little RG;
PI WPI; 1996-179900/18.
DR Antifungal peptide(s) derived from Domain III of BPI protein - used
XX in vitro for killing or inhibiting replication of fungi, esp.
PT Candida species
XX
PS Claim 14; Page 151; 199pp; English.
XX
CC AAW04000-W04160 represent antifungal peptides. These sequences are
CC based on (or derived from) Domain III of the
CC bactericidal/permeability-increasing protein (BPI). BPI is a protein
CC that can be isolated from the granules of mammalian polymorphonuclear
CC leukocytes (PMNs or neutrophils). These antifungal peptides can be used
CC for killing, or inhibiting replication of, fungi in vitro. These
CC sequences can also be used for treatment of a fungal infection involving
CC fungi from the species Candida, Aspergillus and Cryptococcus. The
CC sequences are especially useful for treating C.albicans, C.galabrata,
CC C.krusei, C.lusitanae, C.parapsilosis and C.tropicalis infections.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 33; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
Db 1 WLIQLK 6

RESULT 2
AAW44553
ID AAW44553 standard; peptide: 6 AA.
XX
AC AAW44553;
XX
DT 27-APR-1998 (first entry)
XX
DE Anti-fungal peptide #154 based on BPI protein: (residues 142-169).
DE
XX
KW Anti-fungal peptide; bactericidal-permeability-increasing protein: BPI;
KW polymorphonuclear leukocyte; fungicide.
XX
OS Synthetic.
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Modified-site 6 /note= "C-terminal amide"
FT
XX
PN W09704008-A1.
XX
PD 06-FEB-1997.
XX
XX 21-MAR-1996; 96WO-US03845.
PF
XX 20-JUL-1995; 95US-0504841.
PR
XX (XOMA) XOMA CORP.
PA
XX Fadem MB, Lim E, Little RG;
XX WPI; 1997-132578/12.
DR
XX Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides
XX
PS Claim 1; Page 188; 230pp; English.
XX

CC This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 33; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
Db 1 WLIQLK 6

RESULT 3
AAW43743
ID AAW43743 standard; peptide: 6 AA.
XX
AC AAW43743;
XX
DT 20-APR-1998 (first entry)
XX
DE Bactericidal/permeability increasing peptide xmp.321.
XX
KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW bacterial infection; fungal infection; endotoxin; heparin;
KW angiogenesis; fungicidal; recombinant DNA; vector.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 6 /note= "Amidated"
FT
XX
PN W09735009-A1.
XX
PD 25-SEP-1997.
XX
PF 18-MAR-1997; 97WO-US05287.
XX
PR 22-MAR-1996; 96US-0621803.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD;
XX
DR WPI; 1997-480215/44.
XX
PT Recombinant production of bactericidal/permeability increasing
PT protein - by expression as a fusion protein in microbial host cells,
PT then cleaving the BPI peptide from the carrier
XX
PS Claim 10; Page 123; 186pp; English.
XX
CC A new recombinant DNA vector construct has been developed which encodes
CC a fusion protein and is suitable for introduction into a bacterial host.
CC The vector comprises: (a) DNA encoding at least one cationic
CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC located between (a) and (b). The present sequence represents a
CC specifically claimed BPI peptide. The peptides have many uses including
CC the treatment of bacterial and fungal infections. BPI peptides also
CC bind to endotoxins and heparin, neutralising their effects. The
CC peptides have further been shown to inhibit angiogenesis (partly due to
CC heparin-binding activity). The fusion proteins have been found to be
CC expressed in large amounts without significant proteolysis, and in some
CC cases are actually secreted from the host cells. This allows the

CC indirect production of anti-microbial BPI peptides in microbial hosts.

XX Sequence 6 AA;

Query Match 100.0%; Score 33; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
|||||

Db 1 WLIQLK 6

RESULT 4
AAY00530
ID AAY00530 standard; Peptide; 6 AA.
XX
AC AAY00530;
XX
DT 07-MAY-1999 (first entry)
XX
DE Antifungal peptide XMP.321.
XX
KW Antifungal; BPI; bactericidal/permeability increasing protein;
KW Candida infection.

XX Synthetic.
XX US5858974-A.
PN
XX 12-JAN-1999.
PD
XX 21-MAR-1996; 96US-0621259.
PF
XX 21-MAR-1996; 96US-0621259.
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;
XX
DR WPI; 1999-119956/10.
XX
PT Antifungal peptides - comprising part of bactericidal or
PT permeability-increasing protein sequence or related sequence
XX
PS Disclosure; Columns 161-162; 132pp; English.

XX New peptides are provided which are based on Domain III (amino acids
CC 142-169) of human bactericidal/permeability-increasing protein (BPI).
CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGLIQLFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, IQLF, WLIQL, LIQLF and WLIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of
CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.

XX Sequence 6 AA;

Query Match 100.0%; Score 33; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
|||||

Db 1 WLIQLK 6

RESULT 5
AAB65454
ID AAB65454 standard; Peptide; 6 AA.
XX
AC AAB65454;
XX
DT 27-MAR-2001 (first entry)
XX
DE Anti-fungal peptide XMP.321.
XX

KW Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;
KW bactericidal/permeability-increasing protein; bactericidal;
KW fungal infection.

XX Homo sapiens.
XX
PN US6156730-A.
XX
PD 05-DEC-2000.
XX
PF 08-JAN-1999; 99US-0227659.
XX
PR 21-MAR-1996; 96US-0621259.
PR 12-MAR-1993; 93US-0030644.
PR 15-JUL-1993; 93US-0093202.
PR 14-JAN-1994; 94US-0183222.
PR 11-MAR-1994; 94US-0209762.
PR 11-JUL-1994; 94US-0273540.
PR 15-SEP-1994; 94US-0306473.
PR 13-JAN-1995; 95US-0372105.
PR 20-JUL-1995; 95US-0504841.

XX (XOMA) XOMA CORP.
XX
PI Lim E, Fadem MB, Little RG;
XX
DR WPI; 2001-090160/10.
XX

PI Novel anti-fungal peptides derived from domain III of
PT bactericidal/permeability-increasing protein useful for killing or
PT inhibiting replication of fungi and for treating fungal infections -
XX
PS Example 2; Columns 165-166; 134pp; English.

XX The present invention relates to antifungal peptides (see
CC AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C. albicans, C. glabrata, C. krusei,
CC C. lusitanae, C. parapsilosis and C. tropicalis.

XX Sequence 6 AA;

Query Match 100.0%; Score 33; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
|||||

Db 1 WLIQLK 6

RESULT 6
AAW04025
ID AAW04025 standard; peptide; 7 AA.

XX AAW04025;
AC 31-OCT-1996 (first entry)
XX Antifungal peptide XMP.322.
DE
XX Antifungal peptide; inhibitor; Domain III; polymorphonuclear leukocyte;
KW bactericidal/permeability-increasing protein; BPI; mammalian; PMN; fungi;
KW neutrophil; replication inhibitor; fungal infection; Aspergillus;
KW Cryptococcus; Candida; C.albicans; C.galabrat; C.krusei; C.lusitaniae;
KW C.parapsilosis; C.tropicalis; therapy.
XX Synthetic.
OS
XX
XX Antifungal peptide; inhibitor; Domain III; polymorphonuclear leukocyte;
KW bactericidal/permeability-increasing protein; BPI; mammalian; PMN; fungi;
KW neutrophil; replication inhibitor; fungal infection; Aspergillus;
KW Cryptococcus; Candida; C.albicans; C.galabrat; C.krusei; C.lusitaniae;
KW C.parapsilosis; C.tropicalis; therapy.
XX
OS
XX
XX Key Location/Qualifiers
FT Modified-site 7 /note= "amidated"
FT
XX
PN WO9608509-A1.
XX
XX 21-MAR-1996.
XX
XX 20-JUL-1995; 95WO-US09262.
XX
XX 13-JAN-1995; 95US-0372105.
PR 15-SEP-1994; 94US-0306473.
XX
XX (XOMA) XOMA CORP.
XX
XX Fadem MB, Lim E, Little RG;
PI
XX WPI; 1996-179900/18.
DR
XX Antifungal peptide(s) derived from Domain III of BPI protein - used
PT in vitro for killing or inhibiting replication of fungi, esp.
PT Candida species
XX
XX Claim 5; Page 152; 199pp; English.
PS
XX AAW04000-W04160 represent antifungal peptides. These sequences are
CC based on (or derived from) Domain III of the
CC bactericidal/permeability-increasing protein (BPI). BPI is a protein
CC that can be isolated from the granules of mammalian polymorphonuclear
CC leukocytes (PMNs or neutrophils). These antifungal peptides can be used
CC for killing, or inhibiting replication of, fungi in vitro. These
CC sequences can also be used for treatment of a fungal infection involving
CC fungi from the species Candida, Aspergillus and Cryptococcus. The
CC sequences are especially useful for treating C.albicans, C.galabrat,
CC C.krusei, C.lusitaniae, C.parapsilosis and C.tropicalis infections.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 33; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLIQLK 6
Db 1 WLIQLK 6
RESULT 7
AAW04026
ID AAW04026 standard; peptide; 7 AA.
XX
AC AAW04026;
XX
DT 31-OCT-1996 (first entry)
XX
DE Antifungal peptide XMP.323.
XX
KW Antifungal peptide; inhibitor; Domain III; polymorphonuclear leukocyte;

KW bactericidal/permeability-increasing protein; BPI; mammalian; PMN; fungi;
KW neutrophil; replication inhibitor; fungal infection; Aspergillus;
KW Cryptococcus; Candida; C.albicans; C.galabrat; C.krusei; C.lusitaniae;
KW C.parapsilosis; C.tropicalis; therapy.
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FT Modified-site 7 /note= "amidated"
FT
XX
PN WO9608509-A1.
XX
XX 21-MAR-1996.
XX
XX 20-JUL-1995; 95WO-US09262.
XX
XX 13-JAN-1995; 95US-0372105.
PR 15-SEP-1994; 94US-0306473.
XX
XX (XOMA) XOMA CORP.
XX
XX Fadem MB, Lim E, Little RG;
PI
XX WPI; 1996-179900/18.
DR
XX Antifungal peptide(s) derived from Domain III of BPI protein - used
PT in vitro for killing or inhibiting replication of fungi, esp.
PT Candida species
XX
XX Claim 5; Page 152; 199pp; English.
PS
XX AAW04000-W04160 represent antifungal peptides. These sequences are
CC based on (or derived from) Domain III of the
CC bactericidal/permeability-increasing protein (BPI). BPI is a protein
CC that can be isolated from the granules of mammalian polymorphonuclear
CC leukocytes (PMNs or neutrophils). These antifungal peptides can be used
CC for killing, or inhibiting replication of, fungi in vitro. These
CC sequences can also be used for treatment of a fungal infection involving
CC fungi from the species Candida, Aspergillus and Cryptococcus. The
CC sequences are especially useful for treating C.albicans, C.galabrat,
CC C.krusei, C.lusitaniae, C.parapsilosis and C.tropicalis infections.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 33; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLIQLK 6
Db 2 WLIQLK 7
RESULT 8
AAW44554
ID AAW44554 standard; peptide; 7 AA.
XX
AC AAW44554;
XX
DT 27-APR-1998 (first entry)
XX
DE Anti-fungal peptide #155 based on BPI protein (residues 142-169).
XX
KW Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.
XX
OS Synthetic.
OS Mammalia.
XX
XX Key Location/Qualifiers
FT Modified-site 7 /note= "C-terminal amide"
FT

XX WO9704008-A1.
PN
XX
PD
XX
PF 21-MAR-1996; 96WO-US03845.
XX
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;
XX
DR WPI; 1997-132578/12.
XX
PT Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides
XX
PS Claim 1; Page 189; 230pp; English.
XX
CC This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 33; DB 18; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WLIQLK 6
Db
1 WLIQLK 6
RESULT 9
AAW44555
ID AAW44555 standard; peptide; 7 AA.
XX
AC AAW44555;
XX
DT 27-APR-1998 (first entry)
XX
DE Anti-fungal peptide #156 based on BPI protein (residues 142-169).
XX
KW Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.
XX
OS Synthetic.
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Modified-site 7 /note= "C-terminal amide"
FT
XX
PN WO9704008-A1.
XX
PD 06-FEB-1997.
XX
PF 21-MAR-1996; 96WO-US03845.
XX
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;
XX
DR WPI; 1997-132578/12.

XX Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides
XX
PS Claim 1; Page 189; 230pp; English.
XX
CC This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 33; DB 18; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WLIQLK 6
Db
2 WLIQLK 7
RESULT 10
AAW43746
ID AAW43746 standard; peptide; 7 AA.
XX
AC AAW43746;
XX
DT 20-APR-1998 (first entry)
XX
DE Bactericidal/permeability increasing peptide XMP.324.
XX
KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW bacterial infection; fungal infection; endotoxin; heparin;
KW angiogenesis; fungicidal; recombinant DNA; vector.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 7 /note= "Amidated"
FT
XX
PN WO9735009-A1.
XX
PD 25-SEP-1997.
XX
PF 18-MAR-1997; 97WO-US05287.
XX
PR 22-MAR-1996; 96US-0621803.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD;
XX
DR WPI; 1997-480215/44.
XX
PT Recombinant production of bactericidal/permeability increasing
PT protein - by expression as a fusion protein in microbial host cells,
PT then cleaving the BPI peptide from the carrier
XX
PS Claim 10; Page 124; 186pp; English.
XX
CC A new recombinant DNA vector construct has been developed which encodes
CC a fusion protein and is suitable for introduction into a bacterial host.
CC The vector comprises: (a) DNA encoding at least one cationic
CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC located between (a) and (b). The present sequence represents a

CC specifically claimed BPI peptide. The peptides have many uses including
CC the treatment of bacterial and fungal infections. BPI peptides also
CC bind to endotoxins and heparin, neutralising their effects. The
CC peptides have further been shown to inhibit angiogenesis (partly due to
CC heparin-binding activity). The fusion proteins have been found to be
CC expressed in large amounts without significant proteolysis, and in some
CC cases are actually secreted from the host cells. This allows the
CC indirect production of anti-microbial BPI peptides in microbial hosts.

XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 33; DB 18; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
| | | | |
Db 2 WLIQLK 7

RESULT 11
AAW43744
ID AAW43744 standard; peptide: 7 AA.
XX
AC AAW43744;
XX
DT 20-APR-1998 (first entry)
XX
DE Bactericidal/permeability increasing peptide XMP.322.
XX
KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW bacterial infection; fungal infection; endotoxin; heparin;
KW angiogenesis; fungicidal; recombinant DNA; vector.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 7 /note- "Amidated"
FT
XX
PN WO9735009-A1.
XX
PD 25-SEP-1997.
XX
PF 18-MAR-1997; 97WO-US05287.
XX
PR 22-MAR-1996; 96US-0621803.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD;
XX
DR WPI; 1997-480215/44.
XX
PT Recombinant production of bactericidal/permeability increasing
PT protein - by expression as a fusion protein in microbial host cells,
PT then cleaving the BPI peptide from the carrier
XX
PS Claim 10; Page 124; 186pp; English.
XX
CC A new recombinant DNA vector construct has been developed which encodes
CC a fusion protein and is suitable for introduction into a bacterial host.
CC The vector comprises: (a) DNA encoding at least one cationic
CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC located between (a) and (b). The present sequence represents a
CC specifically claimed BPI peptide. The peptides have many uses including
CC the treatment of bacterial and fungal infections. BPI peptides also
CC bind to endotoxins and heparin, neutralising their effects. The
CC peptides have further been shown to inhibit angiogenesis (partly due to
CC heparin-binding activity). The fusion proteins have been found to be
CC expressed in large amounts without significant proteolysis, and in some

CC cases are actually secreted from the host cells. This allows the
CC indirect production of anti-microbial BPI peptides in microbial hosts.

XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 33; DB 18; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
| | | | |
Db 1 WLIQLK 6

RESULT 12
AAW43745
ID AAW43745 standard; peptide: 7 AA.
XX
AC AAW43745;
XX
DT 20-APR-1998 (first entry)
XX
DE Bactericidal/permeability increasing peptide XMP.323.
XX
KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW bacterial infection; fungal infection; endotoxin; heparin;
KW angiogenesis; fungicidal; recombinant DNA; vector.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 7 /note- "Amidated"
FT
XX
PN WO9735009-A1.
XX
PD 25-SEP-1997.
XX
PF 18-MAR-1997; 97WO-US05287.
XX
PR 22-MAR-1996; 96US-0621803.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD;
XX
DR WPI; 1997-480215/44.
XX
PT Recombinant production of bactericidal/permeability increasing
PT protein - by expression as a fusion protein in microbial host cells,
PT then cleaving the BPI peptide from the carrier
XX
PS Claim 10; Page 124; 186pp; English.
XX
CC A new recombinant DNA vector construct has been developed which encodes
CC a fusion protein and is suitable for introduction into a bacterial host.
CC The vector comprises: (a) DNA encoding at least one cationic
CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC located between (a) and (b). The present sequence represents a
CC specifically claimed BPI peptide. The peptides have many uses including
CC the treatment of bacterial and fungal infections. BPI peptides also
CC bind to endotoxins and heparin, neutralising their effects. The
CC peptides have further been shown to inhibit angiogenesis (partly due to
CC heparin-binding activity). The fusion proteins have been found to be
CC expressed in large amounts without significant proteolysis, and in some
CC cases are actually secreted from the host cells. This allows the
CC indirect production of anti-microbial BPI peptides in microbial hosts.

XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 33; DB 18; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
|||||
Db 2 WLIQLK 7

RESULT 13

AAAY00531
ID AAAY00531 standard; Peptide; 7 AA.

XX AC AAAY00531;

XX DT 07-MAY-1999 (first entry)

XX DE Antifungal peptide XMP.322.

XX KW Antifungal; BPI; bactericidal/permeability increasing protein;
KW Candida infection.

XX OS Synthetic.

XX PN US5858974-A.

XX PD 12-JAN-1999.

XX PF 21-MAR-1996; 96US-0621259.

XX PR 21-MAR-1996; 96US-0621259.

XX PR 20-JUL-1995; 95US-0504841.

XX PA (XOMA) XOMA CORP.

XX PI Fadem MB, Lim E, Little RG;

XX DR WPI; 1999-119956/10.

XX PT Antifungal peptides - comprising part of bactericidal or
PT permeability-increasing protein sequence or related sequence

XX PS Disclosure; Columns 161-162; 132pp; English.

XX CC New peptides are provided which are based on Domain III (amino acids
CC 142-169) of human bactericidal/permeability-increasing protein (BPI).
CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGWLIQLFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, LIQLF, WLIQL, LIQLF and WLIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of
CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 33; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
|||||
Db 1 WLIQLK 6

RESULT 14

AAAY00532

ID AAAY00532 standard; Peptide; 7 AA.

XX AC AAAY00532;

XX DT 07-MAY-1999 (first entry)

XX DE Antifungal peptide XMP.323.

XX KW Antifungal; BPI; bactericidal/permeability increasing protein;
KW Candida infection.

XX OS Synthetic.

XX PN US5858974-A.

XX PD 12-JAN-1999.

XX PF 21-MAR-1996; 96US-0621259.

XX PR 21-MAR-1996; 96US-0621259.

XX PR 20-JUL-1995; 95US-0504841.

XX PA (XOMA) XOMA CORP.

XX PI Fadem MB, Lim E, Little RG;

XX DR WPI; 1999-119956/10.

XX PT Antifungal peptides - comprising part of bactericidal or
PT permeability-increasing protein sequence or related sequence

XX PS Disclosure; Columns 161-162; 132pp; English.

XX CC New peptides are provided which are based on Domain III (amino acids
CC 142-169) of human bactericidal/permeability-increasing protein (BPI).
CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGWLIQLFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, LIQLF, WLIQL, LIQLF and WLIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of
CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 33; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
|||||
Db 2 WLIQLK 7

RESULT 15

AAAB65455

ID AAAB65455 standard; Peptide; 7 AA.

XX AC AAAB65455;

XX DT 27-MAR-2001 (first entry)

XX DE Anti-fungal peptide XMP.322.

XX KW Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;
KW bactericidal/permeability-increasing protein; bactericidal;

KW fungal infection.
XX
OS Homo sapiens.
XX
PN US6156730-A.
XX
PD 05-DEC-2000.
XX
PF 08-JAN-1999; 99US-0227659.
XX
PR 21-MAR-1996; 96US-0621259.
PR 12-MAR-1993; 93US-0030644.
PR 15-JUL-1993; 93US-0093202.
PR 14-JAN-1994; 94US-0183222.
PR 11-MAR-1994; 94US-0209762.
PR 11-JUL-1994; 94US-0273540.
PR 15-SEP-1994; 94US-0306473.
PR 13-JAN-1995; 95US-0372105.
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Lim E, Fadem MB, Little RG;
XX
DR WPI; 2001-090160/10.
XX
PT Novel anti-fungal peptides derived from domain III of
PT bactericidal/permeability-increasing protein useful for killing or
PT inhibiting replication of fungi and for treating fungal infections -
XX
PS Example 2; Columns 165-166; 134pp; English.
XX
CC The present invention relates to antifungal peptides (see
CC AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C.albicans, C.glabrata, C.krusei,
CC C.lusitanae, C.parapsilosis and C.tropicalis.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 33; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
 |||||
Db 1 WLIQLK 6

Search completed: October 14, 2003, 14:41:31
Job time : 26.9167 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:23 ; Search time 8.5 Seconds
(without alignments)
29.866 Million cell updates/sec

Title: US-09-881-490-154
Perfect score: 33
Sequence: i WLIQLK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 33 | 100.0 | 6 | 2 | US-08-621-803-187 |
| 2 | 33 | 100.0 | 6 | 2 | US-08-621-259A-154 |
| 3 | 33 | 100.0 | 6 | 3 | US-09-217-352-187 |
| 4 | 33 | 100.0 | 6 | 5 | PCT-US95-09262-154 |
| 5 | 33 | 100.0 | 7 | 2 | US-08-621-803-188 |
| 6 | 33 | 100.0 | 7 | 2 | US-08-621-803-189 |
| 7 | 33 | 100.0 | 7 | 2 | US-08-621-803-190 |
| 8 | 33 | 100.0 | 7 | 2 | US-08-621-259A-155 |
| 9 | 33 | 100.0 | 7 | 2 | US-08-621-259A-156 |
| 10 | 33 | 100.0 | 7 | 3 | US-09-217-352-188 |
| 11 | 33 | 100.0 | 7 | 3 | US-09-217-352-189 |
| 12 | 33 | 100.0 | 7 | 3 | US-09-217-352-190 |
| 13 | 33 | 100.0 | 7 | 5 | PCT-US95-09262-155 |
| 14 | 33 | 100.0 | 7 | 5 | PCT-US95-09262-156 |
| 15 | 33 | 100.0 | 8 | 2 | US-08-621-803-192 |
| 16 | 33 | 100.0 | 8 | 2 | US-08-621-259A-157 |
| 17 | 33 | 100.0 | 8 | 2 | US-08-621-259A-159 |
| 18 | 33 | 100.0 | 8 | 3 | US-09-217-352-192 |
| 19 | 33 | 100.0 | 8 | 5 | PCT-US95-09262-157 |
| 20 | 33 | 100.0 | 8 | 5 | PCT-US95-09262-159 |
| 21 | 33 | 100.0 | 9 | 2 | US-08-621-803-193 |
| 22 | 33 | 100.0 | 9 | 2 | US-08-621-803-197 |
| 23 | 33 | 100.0 | 9 | 2 | US-08-621-803-198 |
| 24 | 33 | 100.0 | 9 | 2 | US-08-621-259A-160 |
| 25 | 33 | 100.0 | 9 | 2 | US-08-621-259A-162 |
| 26 | 33 | 100.0 | 9 | 2 | US-08-621-259A-164 |
| 27 | 33 | 100.0 | 9 | 2 | US-08-621-259A-165 |

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| 28 | 33 | 100.0 | 9 | 2 | US-08-621-259A-166 | Sequence 166, App |
| 29 | 33 | 100.0 | 9 | 2 | US-08-621-259A-173 | Sequence 173, App |
| 30 | 33 | 100.0 | 9 | 3 | US-09-217-352-193 | Sequence 193, App |
| 31 | 33 | 100.0 | 9 | 3 | US-09-217-352-197 | Sequence 197, App |
| 32 | 33 | 100.0 | 9 | 3 | US-09-217-352-198 | Sequence 198, App |
| 33 | 33 | 100.0 | 9 | 5 | PCT-US95-09262-160 | Sequence 160, App |
| 34 | 33 | 100.0 | 9 | 5 | PCT-US95-09262-162 | Sequence 162, App |
| 35 | 33 | 100.0 | 9 | 5 | PCT-US95-09262-164 | Sequence 164, App |
| 36 | 33 | 100.0 | 9 | 5 | PCT-US95-09262-165 | Sequence 165, App |
| 37 | 33 | 100.0 | 9 | 5 | PCT-US95-09262-166 | Sequence 166, App |
| 38 | 33 | 100.0 | 9 | 5 | PCT-US95-09262-173 | Sequence 173, App |
| 39 | 33 | 100.0 | 10 | 2 | US-08-621-803-204 | Sequence 204, App |
| 40 | 33 | 100.0 | 10 | 2 | US-08-621-803-205 | Sequence 205, App |
| 41 | 33 | 100.0 | 10 | 2 | US-08-621-259A-179 | Sequence 179, App |
| 42 | 33 | 100.0 | 10 | 2 | US-08-621-259A-180 | Sequence 180, App |
| 43 | 33 | 100.0 | 10 | 3 | US-09-217-352-204 | Sequence 204, App |
| 44 | 33 | 100.0 | 10 | 3 | US-09-217-352-205 | Sequence 205, App |
| 45 | 33 | 100.0 | 10 | 5 | PCT-US95-09262-179 | Sequence 179, App |

ALIGNMENTS

RESULT 1
US-08-621-803-187
: Sequence 187, Application US/08621803
: Patent No. 5851802
: GENERAL INFORMATION:
: APPLICANT: Better, Marc D.
: TITLE OF INVENTION: Methods for Recombinant Microbial Production of
: TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
: NUMBER OF SEQUENCES: 265
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/621,803
: FILING DATE: 22-MAR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Borun, Michael F.
: REGISTRATION NUMBER: 25,447
: REFERENCE/DOCKET NUMBER: 27129/33199
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 187:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: *XMP.321*
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: C-Terminus
: OTHER INFORMATION: /label= Amidation
: OTHER INFORMATION: /note= "The C-terminus is Amidated."
US-08-621-803-187

Query Match 100.0%; Score 33; DB 2: Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLIQLK 6
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Db 1 WLIQLK 6

RESULT 2
US-08-621-259A-154
; Sequence 154, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little IL, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 154:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.321"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-154

Query Match 100.0%; Score 33; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLIQLK 6
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Db 1 WLIQLK 6

RESULT 3
US-09-217-352-187
; Sequence 187, Application US/09217352
; Patent No. 6274344
; GENERAL INFORMATION:
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; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,352
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 187:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.321"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-09-217-352-187

Query Match 100.0%; Score 33; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLIQLK 6
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Db 1 WLIQLK 6

RESULT 4
PCI-US95-09262-154
; Sequence 154, Application PC/TUS9509262
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09262
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/306,473
; FILING DATE: 15-SEP-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/209,762
; FILING DATE: 11-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/10040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 154:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.321"
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; OTHER INFORMATION: /label= Amidation
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PCT-US95-09262-154
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Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLIQLK 6
Db 1 WLIQLK 6
RESULT 5
US-08-621-803-188
; Sequence 188, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
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; ZIP: 60606-6402
; COMPUTER READABLE FORM:
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
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; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-803-188
Query Match 100.0%; Score 33; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLIQLK 6
Db 1 WLIQLK 6
RESULT 6
US-08-621-803-189
; Sequence 189, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
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;   TELEX: 25-3856
;   INFORMATION FOR SEQ ID NO: 189:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 7 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     FEATURE:
;       NAME/KEY: misc_feature
;       OTHER INFORMATION: "XMP.323"
;     FEATURE:
;       NAME/KEY: Modified-site
;       LOCATION: C-Terminus
;       OTHER INFORMATION: /label= Amidation
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US-08-621-803-189
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Query Match          100.0%; Score 33; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. NO. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 WLIQLK 6
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Db       2 WLIQLK 7
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RESULT 7
US-08-621-803-190
; Sequence 190, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
;   APPLICANT: Better, Marc D.
;   TITLE OF INVENTION: Methods for Recombinant Microbial Production of
;   FUSION PROTEINS AND BPI-DERIVED PEPTIDES
;   NUMBER OF SEQUENCES: 265
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;     STREET: 6300 Sears Tower, 233 South Wacker Drive
;     CITY: Chicago
;     STATE: Illinois
;     COUNTRY: United States of America
;     ZIP: 60606-6402
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/621,803
;     FILING DATE: 22-MAR-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Borun, Michael F.
;       REGISTRATION NUMBER: 25,447
;       REFERENCE/DOCKET NUMBER: 27129/33199
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 312/474-6300
;       TELEFAX: 312/474-0448
;       TELEX: 25-3856
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; INFORMATION FOR SEQ ID NO: 190:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 7 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;     NAME/KEY: misc_feature
;     OTHER INFORMATION: "XMP.324"
;   FEATURE:
;     NAME/KEY: Modified-site
;     LOCATION: C-Terminus
;     OTHER INFORMATION: /label= Amidation
;     OTHER INFORMATION: /note= "The C-Terminus is Amidated."
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US-08-621-803-190
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Query Match          100.0%; Score 33; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. NO. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db       2 WLIQLK 7
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RESULT 8
US-08-621-259A-155
; Sequence 155, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
;   APPLICANT: Little II, Roger G
;   APPLICANT: Lim, Edward
;   APPLICANT: Fadem, Mitchell B.
;   TITLE OF INVENTION: Anti-Fungal Peptides
;   NUMBER OF SEQUENCES: 252
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;     STREET: 500 West Madison Street
;     CITY: Chicago
;     STATE: Illinois
;     COUNTRY: United States of America
;     ZIP: 60661
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/621,259A
;     FILING DATE: 21-MAR-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/504,841
;     FILING DATE: 20-JUL-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME: McNicholas, Janet M.
;       REGISTRATION NUMBER: 32,918
;       REFERENCE/DOCKET NUMBER: 11021US02
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 312/707-8889
;       TELEFAX: 312/707-9155
;       TELEX:
;
; INFORMATION FOR SEQ ID NO: 155:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 7 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;     NAME/KEY: misc_feature
;     OTHER INFORMATION: "XMP.322"
;   FEATURE:
;     NAME/KEY: Modified-site
;     LOCATION: C-Terminus
;     OTHER INFORMATION: /label= Amidation
;     OTHER INFORMATION: /note= "The C-Terminus is Amidated."
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US-08-621-259A-155
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Query Match          100.0%; Score 33; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. NO. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 WLIQLK 6
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Db       1 WLIQLK 6
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RESULT 9
US-08-621-259A-156
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; Sequence 156, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621.259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 156:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peplide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.323"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-156

Query Match 100.0%; Score 33; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
Db 2 WLIQLK 7

RESULT 10
US-09-217-352-188
; Sequence 188, Application US/09217352
; Patent No. 6274344
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois

; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,352
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.322"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-09-217-352-188

Query Match 100.0%; Score 33; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
Db 1 WLIQLK 6

RESULT 11
US-09-217-352-189
; Sequence 189, Application US/09217352
; Patent No. 6274344
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,352
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: 22-MAR-1996

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; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.323"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-09-217-352-189

Query Match 100.0%; Score 33; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
Db 2 WLIQLK 7

RESULT 12
US-09-217-352-190
; Sequence 190, Application US/09217352
; Patent No. 6274344
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,352
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 190:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.324"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-09-217-352-190

Query Match 100.0%; Score 33; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
Db 2 WLIQLK 7

RESULT 13
PCT-US95-09262-155
; Sequence 155, Application PC/TUS9509262
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09262
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/10040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.322"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-155

Query Match 100.0%; Score 33; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
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Db 1 WLIQLK 6

RESULT 14
PCT-US95-09262-156
Sequence 156, Application PC/TJS9509262
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Anti-Fungal Peptides
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09262
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/372,105
FILING DATE: 13-JAN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/306,473
FILING DATE: 15-SEP-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/093,202
FILING DATE: 15-JUL-93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030,614
FILING DATE: 12-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/10040
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448

TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.323"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-156

Query Match 100.0%; Score 33; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
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Db 2 WLIQLK 7

RESULT 15
US-08-621-803-192
Sequence 192, Application US/08621803
Patent No. 5851802
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,803
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 192:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.326"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-803-192

Query Match 100.0%; Score 33; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLIQLK 6
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Db 3 WLIQLK 8

Search completed: October 14, 2003, 14:42:45
Job time : 8.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:34:14 ; Search time 14.625 Seconds
(without alignments)
66.104 Million cell updates/sec

Title: US-09-881-490-154
Perfect score: 33
Sequence: 1 WLIQFK 6
Scoring table: BLOSUM62
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Searched: 600653 seqs, 161128416 residues

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Minimum DB seq length: 0
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Listing first 45 summaries

Database : Published_Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
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| 1 | 33 | 100.0 | 6 | 9 US-09-765-527-187 | Sequence 187, App |
| 2 | 33 | 100.0 | 6 | 9 US-09-881-490-154 | Sequence 154, App |
| 3 | 33 | 100.0 | 7 | 9 US-09-765-527-188 | Sequence 188, App |
| 4 | 33 | 100.0 | 7 | 9 US-09-765-527-189 | Sequence 189, App |
| 5 | 33 | 100.0 | 7 | 9 US-09-765-527-190 | Sequence 190, App |
| 6 | 33 | 100.0 | 7 | 9 US-09-881-490-155 | Sequence 155, App |
| 7 | 33 | 100.0 | 7 | 9 US-09-881-490-156 | Sequence 156, App |
| 8 | 33 | 100.0 | 8 | 9 US-09-765-527-192 | Sequence 192, App |
| 9 | 33 | 100.0 | 8 | 9 US-09-881-490-157 | Sequence 157, App |
| 10 | 33 | 100.0 | 8 | 9 US-09-881-490-159 | Sequence 159, App |
| 11 | 33 | 100.0 | 9 | 9 US-09-765-527-193 | Sequence 193, App |
| 12 | 33 | 100.0 | 9 | 9 US-09-765-527-197 | Sequence 197, App |
| 13 | 33 | 100.0 | 9 | 9 US-09-765-527-198 | Sequence 198, App |
| 14 | 33 | 100.0 | 9 | 9 US-09-881-490-160 | Sequence 160, App |
| 15 | 33 | 100.0 | 9 | 9 US-09-881-490-162 | Sequence 162, App |

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|----|----|-------|------|-----------------------|-------------------|
| 16 | 33 | 100.0 | 9 | 9 US-09-881-490-164 | Sequence 164, App |
| 17 | 33 | 100.0 | 9 | 9 US-09-881-490-165 | Sequence 165, App |
| 18 | 33 | 100.0 | 9 | 9 US-09-881-490-166 | Sequence 166, App |
| 19 | 33 | 100.0 | 9 | 9 US-09-881-490-173 | Sequence 173, App |
| 20 | 33 | 100.0 | 10 | 9 US-09-765-527-204 | Sequence 204, App |
| 21 | 33 | 100.0 | 10 | 9 US-09-765-527-205 | Sequence 205, App |
| 22 | 33 | 100.0 | 10 | 9 US-09-881-490-179 | Sequence 179, App |
| 23 | 33 | 100.0 | 10 | 9 US-09-881-490-180 | Sequence 180, App |
| 24 | 33 | 100.0 | 11 | 9 US-09-765-527-206 | Sequence 206, App |
| 25 | 33 | 100.0 | 11 | 9 US-09-881-490-181 | Sequence 181, App |
| 26 | 30 | 90.9 | 9 | 9 US-09-765-527-199 | Sequence 199, App |
| 27 | 30 | 90.9 | 9 | 9 US-09-881-490-167 | Sequence 167, App |
| 28 | 29 | 87.9 | 620 | 10 US-09-965-602-58 | Sequence 58, Appl |
| 29 | 29 | 87.9 | 1160 | 9 US-09-815-242-13913 | Sequence 13913, A |
| 30 | 28 | 84.8 | 5 | 9 US-09-765-527-186 | Sequence 186, App |
| 31 | 28 | 84.8 | 5 | 9 US-09-881-490-153 | Sequence 153, App |
| 32 | 28 | 84.8 | 5 | 9 US-09-881-490-209 | Sequence 209, App |
| 33 | 28 | 84.8 | 6 | 9 US-09-765-527-181 | Sequence 181, App |
| 34 | 28 | 84.8 | 6 | 9 US-09-765-527-182 | Sequence 182, App |
| 35 | 28 | 84.8 | 6 | 9 US-09-765-527-183 | Sequence 183, App |
| 36 | 28 | 84.8 | 6 | 9 US-09-881-490-148 | Sequence 148, App |
| 37 | 28 | 84.8 | 6 | 9 US-09-881-490-149 | Sequence 149, App |
| 38 | 28 | 84.8 | 6 | 9 US-09-881-490-211 | Sequence 211, App |
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| 40 | 28 | 84.8 | 7 | 9 US-09-765-527-174 | Sequence 174, App |
| 41 | 28 | 84.8 | 7 | 9 US-09-765-527-175 | Sequence 175, App |
| 42 | 28 | 84.8 | 7 | 9 US-09-765-527-191 | Sequence 191, App |
| 43 | 28 | 84.8 | 7 | 9 US-09-881-490-140 | Sequence 140, App |
| 44 | 28 | 84.8 | 7 | 9 US-09-881-490-141 | Sequence 141, App |
| 45 | 28 | 84.8 | 7 | 9 US-09-881-490-142 | Sequence 142, App |

ALIGNMENTS

RESULT 1
US-09-765-527-187
; Sequence 187, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 187:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: "XMP.321"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 187:
US-09-765-527-187

Query Match      100.0%; Score 33; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. NO. 5.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WLIQLK 6
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Db      1 WLIQLK 6

RESULT 2
US-09-881-490-154
; Sequence 154, Application US/09881490
; Patent No. JS20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th Floor Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
```

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; INFORMATION FOR SEQ ID NO: 154:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: "XMP.321"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 154:
US-09-881-490-154

Query Match      100.0%; Score 33; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. NO. 5.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WLIQLK 6
      |||||
Db      1 WLIQLK 6

RESULT 3
US-09-765-527-188
; Sequence 188, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: "XMP.322"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
```



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;
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
;
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
;
; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.322"
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; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 155:
US-09-881-490-155

Query Match 100.0%; Score 33; DB 9; Length 7:
Best Local Similarity 100.0%; Pred. No. 5.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLIQLK 6
Db 1 WLIQLK 6

RESULT 7
US-09-881-490-156
; Sequence 156, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
```

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;
;
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
;
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
;
; INFORMATION FOR SEQ ID NO: 156:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.323"
;
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 156:
US-09-881-490-156

Query Match 100.0%; Score 33; DB 9; Length 7:
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLIQLK 6
Db 2 WLIQLK 7

RESULT 8
US-09-765-527-192
; Sequence 192, Application US/09765527
; Patent No. US20020006638A1
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;
;
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
;
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
;
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.326"
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated"
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 159:
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; US-09-881-490-159
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; Query Match 100.0%; Score 33; DB 9; Length 8;
; Best Local Similarity 100.0%; Pred. No. 5.3e+05;
; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 WLIQLK 6
; Db 3 WLIQLK 8
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; RESULT 11
; US-09-765-527-193
; Sequence 193, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
;
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
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```
;
;
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.327"
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated."
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 193:
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; US-09-765-527-193
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; Query Match 100.0%; Score 33; DB 9; Length 9;
; Best Local Similarity 100.0%; Pred. No. 5.3e+05;
; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 WLIQLK 6
; Db 3 WLIQLK 8
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; RESULT 12
; US-09-765-527-197
; Sequence 197, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
;
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 197:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.331"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= Acetylated
/note= "Position 1 is acetylated."
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
/note= "The C-Terminus is Amidated."
SEQUENCE DESCRIPTION: SEQ ID NO: 197:
US-09-765-527-197

Query Match 100.0%; Score 33; DH 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLIQLK 6
Db 3 WLIQLK 8

RESULT 13
US-09-765-527-198
Sequence 198, Application US/09/765527
Patent No. US2002000638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.

REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 198:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.335"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
/note= "The C-Terminus is Amidated."
SEQUENCE DESCRIPTION: SEQ ID NO: 198:
US-09-765-527-198
Query Match 100.0%; Score 33; DH 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WLIQLK 6
Db 3 WLIQLK 8
RESULT 14
US-09-881-490-160
Sequence 160, Application US/09881490
Patent No. US2002007298A1
GENERAL INFORMATION:
APPLICANT: Little II, Roger G.
Lim, Edward
Faden, Mitchell B.
TITLE OF INVENTION: Anti-Fungal Peptides
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th FloorDrive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/881,490
FILING DATE: 14-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/119,858
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/372,105
FILING DATE: 13-JAN-95
APPLICATION NUMBER: 08/306,473
FILING DATE: 15-SEP-94
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-94
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-94
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-94
APPLICATION NUMBER: 08/093,202
FILING DATE: 15-JUL-93
APPLICATION NUMBER: 08/030,644

; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.327"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 160:
US-09-881-490-160

Query Match 100.0%; Score 33; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
Db 3 WLIQLK 8

RESULT 15
US-09-881-490-162
; Sequence 162, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #2.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94

; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.331"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetylated
; /note= "Position 1 is acetylated"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-09-881-490-162

Query Match 100.0%; Score 33; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
Db 3 WLIQLK 8

Search completed: October 14, 2003, 14:44:49
Job time : 14.625 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 : Search time 7.875 Seconds
(without alignments)
73.271 Million cell updates/sec

Title: US-09-881-490-154
Perfect score: 33
Sequence: 1 WLQLK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 32 | 97.0 | 182 | 2 A90193 | conserved hypothe |
| 2 | 29 | 87.9 | 207 | 2 G84983 | 5-amino-6-(5-phosp |
| 3 | 29 | 87.9 | 287 | 2 B90540 | conserved hypothe |
| 4 | 29 | 87.9 | 341 | 1 E64444 | hypothetical prote |
| 5 | 29 | 87.9 | 388 | 1 WMLJBT | bel-2 protein - si |
| 6 | 29 | 87.9 | 390 | 2 I38370 | hypothetical prote |
| 7 | 29 | 87.9 | 416 | 2 T02194 | probable pectinase |
| 8 | 29 | 87.9 | 420 | 2 T47998 | pectinacetyltera |
| 9 | 29 | 87.9 | 422 | 2 T01197 | pectin acetylster |
| 10 | 29 | 87.9 | 620 | 2 S56790 | probable membranc |
| 11 | 29 | 87.9 | 756 | 2 G86308 | Similar to diseasc |
| 12 | 29 | 87.9 | 1160 | 1 A45915 | DNA-directed DNA p |
| 13 | 29 | 87.9 | 1160 | 2 A10530 | DNA polymerase III |
| 14 | 28 | 84.8 | 59 | 2 AE2023 | hypothetical prote |
| 15 | 28 | 84.8 | 62 | 2 A86805 | hypothetical prote |
| 16 | 28 | 84.8 | 146 | 2 B86721 | transcription regu |
| 17 | 28 | 84.8 | 162 | 2 T02072 | probable glycine c |
| 18 | 28 | 84.8 | 166 | 2 I37052 | H+-transporting tw |
| 19 | 28 | 84.8 | 179 | 2 T43508 | hypothetical prote |
| 20 | 28 | 84.8 | 180 | 1 GCHU | glucagon precursor |
| 21 | 28 | 84.8 | 180 | 1 GCGP | glucagon precursor |
| 22 | 28 | 84.8 | 180 | 1 GCRTDU | glucagon precursor |
| 23 | 28 | 84.8 | 180 | 1 GCRT | glucagon precursor |
| 24 | 28 | 84.8 | 180 | 1 GCHV | glucagon precursor |
| 25 | 28 | 84.8 | 180 | 2 A57294 | glucagon precursor |
| 26 | 28 | 84.8 | 189 | 2 AH1029 | probable membrane |
| 27 | 28 | 84.8 | 194 | 2 PC1136 | amidophosphoribosy |
| 28 | 28 | 84.8 | 207 | 2 T32983 | hypothetical prote |
| 29 | 28 | 84.8 | 215 | 2 C70471 | hypothetical prote |

| | | | | | |
|----|----|------|-----|----------|--------------------|
| 30 | 28 | 84.8 | 215 | 2 AE2177 | hypothetical prote |
| 31 | 28 | 84.8 | 226 | 2 T11838 | H+-transporting tw |
| 32 | 28 | 84.8 | 226 | 2 T11498 | H+-transporting tw |
| 33 | 28 | 84.8 | 226 | 2 S26156 | H+-transporting tw |
| 34 | 28 | 84.8 | 226 | 2 S41840 | H+-transporting tw |
| 35 | 28 | 84.8 | 226 | 2 T10977 | H+-transporting tw |
| 36 | 28 | 84.8 | 226 | 2 F59153 | H+-transporting tw |
| 37 | 28 | 84.8 | 230 | 2 T45555 | H+-transporting tw |
| 38 | 28 | 84.8 | 250 | 4 S43383 | bactericidal/perme |
| 39 | 28 | 84.8 | 275 | 2 H81074 | phytoene synthase |
| 40 | 28 | 84.8 | 276 | 2 D81868 | probable transfera |
| 41 | 28 | 84.8 | 292 | 2 A64624 | hypothetical prote |
| 42 | 28 | 84.8 | 326 | 2 T26368 | hypothetical prote |
| 43 | 28 | 84.8 | 368 | 2 T47894 | actin-like protein |
| 44 | 28 | 84.8 | 379 | 2 AG3355 | membrane metallopr |
| 45 | 28 | 84.8 | 394 | 2 S76353 | probable aspartate |

ALIGNMENTS

RESULT 1

A90193
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: A90193
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Ailard, G.; Awayez, M.J.;
Jong, J.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redd
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: A90193
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-182 <KUR>
A:Cross-references: GB:AE006641; NID:gl3813634; PIDN:AAK40800.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO0479

Query Match 97.0%; Score 32; DB 2; Length 182;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLQLK 6
|||
Db 110 WLVLK 115

RESULT 2

G84983
5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193) [imported] - Buchn
N:Alternate names: riboflavin reductase
C:Species: Buchnera sp.
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: G84983
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera
A:Reference number: A84930; MUID:20445173; PMID:10993077
A:Accession: G84983
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-207 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: ribD2; BU462
C:Keywords: oxidoreductase
Query Match 87.9%; Score 29; DB 2; Length 207;
Best Local Similarity 83.3%; Pred. No. 66;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
|||:|

Db 90 WLIRLK 95

RESULT 3
B90540
conserved hypothetical protein MYPU_2260 [imported] - Mycoplasma pulmonis (strain UAH CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: B90540
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
A:Reference number: A95512; MUID:21267165; PMID:11353084
A:Accession: B90540
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-287 <KUR>
A:Cross-references: GR:AL445566; PID:gl4089639; PIDN:CAC13399.1; GSPDB:GN00153
A:Experimental source: Strain UAH CTIP
C:Genetics:
A:Gene: MYPU_2260
A:Genetic code: SGC3

Query Match 87.9%; Score 29; DB 2; Length 287;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
|||:|

Db 272 WLIRLK 277

RESULT 4
E64444
hypothetical protein MJ1157 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: E64444
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.;
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
Rosen, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.G.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: E64444
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-341 <RUL>
A:Cross-references: GB:U67558; GB:L77117; NID:ql591786; PIDN:AAB99161.1; PID:ql592323;
C:Genetics:
A:Map position: FOR1097616-1098641
C:Superfamily: conserved hypothetical protein MJ1157

Query Match 87.9%; Score 29; DB 1; Length 341;
Best Local Similarity 83.3%; Pred. No. 11e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
|||:|

Db 333 WLIRLK 338

RESULT 5
WMLJBT
bel-2 protein - simian foamy virus (type 3, strain LK3)
C:Species: simian foamy virus
A:Note: host (African green monkey)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Apr-1994

C:Accession: E40820
R:Renne, R.; Friedl, E.; Schweizer, M.; Fleps, U.; Turek, R.; Neumann-Haefelin, D.
Virology 186, 597-608, 1992
A:Title: Genomic organization and expression of simian foamy virus type 3 (SFV-3).
A:Reference number: A40820; MUID:92124734; PMID:1310187
A:Accession: E40820
A:Molecule type: DNA
A:Residues: 1-388 <REN>
A:Cross-references: GB:M74895
C:Genetics:
A:Gene: bel-2
C:Superfamily: foamy virus bel-2 protein

Query Match 87.9%; Score 29; DB 1; Length 388;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
|||:|

Db 182 WLIRLK 187

RESULT 6
T38370
hypothetical protein SPAC25A8.02 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C:Accession: T38370
R:Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, February 1998
A:Reference number: 221789
A:Accession: T38370
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-390 <SKE>
A:Cross-references: EMBL:AL021809; PIDN:CAA16952.1; GSPDB:GN00066; SPDB:SPAC25A8.02
A:Experimental source: strain 972h-; cosmid c25A8
C:Genetics:
A:Gene: SPDB:SPAC25A8.02
A:Map position: 1
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC25A8.02

Query Match 87.9%; Score 29; DB 2; Length 390;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
|||:|

Db 333 WLIRLK 338

RESULT 7
T02194
probable pectinacetylesterase At2g46930 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 02-Feb-2001
C:Accession: T02194; A84909
R:Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.;
submitted to the EMBL Data Library, September 1998
A:Description: Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence.
A:Reference number: 214603
A:Accession: T02194
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-416 <ROU>
A:Cross-references: EMBL:AC004411; NID:g3522932; PID:g3522956
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallor
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vente
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: AB4909
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-416 <STO>
A;Cross-references: GB:AE002093; NID:g3522956; PIDN:AAC34238.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g46930; F14M4.24
A;Map position: 2
A;Introns: 67/1; 94/3; 138/1; 162/3; 191/3; 233/2; 253/3; 271/3; 297/3; 333/1; 381/3

Query Match 87.9%; Score 29; DB 2; Length 416;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLIQLK 6
| | | | |
Db 89 WLIQLE 94

RESULT 8
T47998
pectinacetylsterase-like protein T17J13.20 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C;Accession: T47998
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24482
A;Accession: T47998
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-420 <RIE>
A;Cross-references: EMBL:AL138651
A;Experimental source: cultivar Columbia; BAC clone T17J13
C;Genetics:
A;Map position: 3
A;Introns: 69/1; 96/3; 140/1; 164/3; 202/1; 236/2; 256/3; 274/3; 300/3; 336/1; 384/3
A;Note: T17J13.20

Query Match 87.9%; Score 29; DB 2; Length 420;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLIQLK 6
| | | | |
Db 91 WLIQLE 96

RESULT 9
T01197
pectin acetylsterase homolog F21E10.11 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
C;Accession: T01197
R;Davidson, S.; Rohlfing, T.; David, M.; O'Brian, D. submitted to the EMBL Data Library, April 1998
A;Description: The sequence of A. thaliana F21E10.
A;Reference number: Z14258
A;Accession: T01197
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-422 <DAV>
A;Cross-references: EMBL:AF058914; NID:g3047074; PID:g3047082; GSPDB:GN00063; ATSP:F21E10
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: ATSP:F21E10.11
A;Map position: 5
A;Introns: 67/1; 94/3; 138/1; 162/3; 191/3; 233/2; 252/3; 277/3; 303/3; 339/1; 387/3

Query Match 87.9%; Score 29; DB 2; Length 422;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLIQLK 6
| | | | |
Db 89 WLIQLE 94

RESULT 10
S56790
probable membrane protein YJL019w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein J1310
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 19-Apr-2002
C;Accession: S56790
R;To Van, D.; Perea, J.; Jacq, C. submitted to the Protein Sequence Database, September 1995
A;Reference number: S56776
A;Accession: S56790
A;Molecule type: DNA
A;Residues: 1-620 <DEH>
A;Cross-references: EMBL:Z49294; NID:q1006737; PID:q1006738; GSPDB:GN00010; MIPS:YJ1
C;Genetics:
A;Gene: MIPS:YJL019w
A;Cross-references: SGD:S0003556
A;Map position: 10L
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YJL019w
C;Keywords: transmembrane protein

Query Match 87.9%; Score 29; DB 2; Length 620;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WLIQLK 6
| | | | |
Db 579 WFIQLK 584

RESULT 11
G86308
Similar to disease resistance proteins [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: G86308
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alcin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86308
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-756 <STO>
A;Cross-references: GB:AE005172; NID:g5734745; PIDN:AAD50010.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

Query Match 87.9%; Score 29; DB 2; Length 756;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLIQLK 6
| | | | |
Db 494 WLIKLK 499

RESULT 12
A45915
DNA-directed DNA polymerase (EC 2.7.7.7) III alpha chain - Salmonella typhimurium
C;Species: Salmonella typhimurium

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jul-2002
C/Accession: A45915
R:Lancy, E.D.; Lifshits, M.R.; Munson, P.; Maurer, R.
J. Bacteriol. 171, 5581-5586, 1989
A/Title: Nucleotide sequence of dnaE, the gene for the polymerase subunit of DNA polymerase III.
A/Reference number: A45915; MUID:90008797; PMID:2676978
A/Accession: A45915
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-1160 <LAN>
A/Cross-references: GB:M29701; NID:q153951; PIDN:AAA27057.1; PID:q153952
C/Superfamily: DNA-directed DNA polymerase III alpha chain
C/Keywords: hydrolase; nucleotidyltransferase

Query Match 87.9%; Score 29; DB 1; Length 1160;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLIQLK 6
||:|
Db 120 WLVELK 125

RESULT 13
A10530
DNA polymerase III, alpha chain [imported] - Salmonella enterica subsp. enterica serovar typhi
C/Species: Salmonella enterica subsp. enterica serovar typhi
C/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: A10530
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, K.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar typhi
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: A10530
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1160 <PAR>
A/Cross-references: GB:AB513382; PIDN:CAD08689.1; PID:q16501512; GSPDB:GN00176
C/Genetics:
A/Gene: STY0254
C/Superfamily: DNA-directed DNA polymerase III alpha chain

Query Match 87.9%; Score 29; DB 2; Length 1160;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLIQLK 6
||:|
Db 120 WLVELK 125

RESULT 14
AE2023
hypothetical protein asl1739 [imported] - Nostoc sp. (strain PCC 7120);
C/Species: Nostoc sp. PCC 7120
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C/Accession: AE2023
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Triguera, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A/Reference number: AB1807; MUID:21595285; PMID:11753840
A/Accession: AE2023
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-59 <KUR>
A/Cross-references: GB:BA000019; PIDN:BA073438.1; PID:q17130829; GSPDB:GN00179

A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: asl1739

Query Match 84.8%; Score 28; DB 2; Length 59;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLIQLK 6
||:|
Db 49 WLVLK 54

RESULT 15
A86805
hypothetical protein yogE [imported] - Lactococcus lactis subsp. lactis (strain IL14)
C/Species: Lactococcus lactis subsp. lactis
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C/Accession: A86805
R:Polot, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; E.
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A/Reference number: A86625; MUID:21235186; PMID:11337471
A/Accession: A86805
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-62 <STO>
A/Cross-references: GB:AE005176; PID:q12724431; PIDN:AAK05539.1; GSPDB:GN00146
A/Experimental source: strain IL1403
C/Genetics:
A/Gene: yogE

Query Match 84.8%; Score 28; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLIQL 5
|||
Db 35 WLVL 39

Search completed: October 14, 2003, 14:38:01
Job time : 9.875 secs

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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 : Search time 4.25 Seconds
(without alignments)
66.391 Million cell updates/sec

Title: US-09-881-490-154
Perfect score: 33
Sequence: 1 WLIQLK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwlssProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 29 | 87.9 | 207 | 1 RID2_BUCAI | P57534 buchnera ap |
| 2 | 29 | 87.9 | 341 | 1 YB57_METJA | Q58558 methanococc |
| 3 | 29 | 87.9 | 388 | 1 YBL2_SFV3L | P27403 simian foam |
| 4 | 29 | 87.9 | 620 | 1 YJB9_YEAST | P47069 saccharomyc |
| 5 | 29 | 87.9 | 1160 | 1 DP3A_SALTY | P14567 salmonella |
| 6 | 28 | 84.8 | 162 | 1 GCSH_ORYSA | Q22535 oryza sativ |
| 7 | 28 | 84.8 | 174 | 1 NUGC_MESVI | Q9mur1 mesostigma |
| 8 | 28 | 84.8 | 180 | 1 GLUC_CAVPO | P05110 cavia porce |
| 9 | 28 | 84.8 | 180 | 1 GLUC_HUMAN | P01275 homo sapien |
| 10 | 28 | 84.8 | 180 | 1 GLUC_MESAU | P01273 mesocricetu |
| 11 | 28 | 84.8 | 180 | 1 GLUC_MOUSE | P55095 mus musculu |
| 12 | 28 | 84.8 | 180 | 1 GLUC_OCTDH | P22890 octodon deg |
| 13 | 28 | 84.8 | 180 | 1 GLUC_RAT | P06883 rattus norv |
| 14 | 28 | 84.8 | 194 | 1 PUR1_LACCA | P35853 lactobacill |
| 15 | 28 | 84.8 | 209 | 1 RYL2_YARLI | P41925 yarrowia li |
| 16 | 28 | 84.8 | 226 | 1 ATP6_CANFA | Q92262 canis famil |
| 17 | 28 | 84.8 | 226 | 1 ATP6_HALGR | P38591 halichoerus |
| 18 | 28 | 84.8 | 226 | 1 ATP6_HIPAM | Q92zy6 hippopotamu |
| 19 | 28 | 84.8 | 226 | 1 ATP6_HYLLA | Q95706 hylobates l |
| 20 | 28 | 84.8 | 226 | 1 ATP6_PHOVI | Q00521 phoca vitul |
| 21 | 28 | 84.8 | 226 | 1 ATP6_PIG | Q35915 sus scrofa |
| 22 | 28 | 84.8 | 257 | 1 NUDC_ECOL6 | Q8fb75 escherichia |
| 23 | 28 | 84.8 | 371 | 1 YB2X_HAEIN | Q86233 haemophilus |
| 24 | 28 | 84.8 | 379 | 1 Y829_BRUME | Q8yhh1 brucella me |
| 25 | 28 | 84.8 | 431 | 1 RAM1_YEAST | P22007 saccharomyc |
| 26 | 28 | 84.8 | 434 | 1 CEMA_MARPO | P12211 marchantia |
| 27 | 28 | 84.8 | 482 | 1 BPI_BOVIN | P17453 bos taurus |
| 28 | 28 | 84.8 | 483 | 1 BPI_HUMAN | P17213 homo sapien |
| 29 | 28 | 84.8 | 547 | 1 YOJI_ECOLI | P33941 escherichia |
| 30 | 28 | 84.8 | 576 | 1 DSRD_PASMU | Q9cp40 pasteurella |
| 31 | 28 | 84.8 | 672 | 1 YCDR_ECOLI | P75906 escherichia |
| 32 | 28 | 84.8 | 910 | 1 SYV_SYNY3 | Q55522 synechocyst |
| 33 | 28 | 84.8 | 1105 | 1 YEGE_ECOLI | P38097 escherichia |

| | | | | | |
|----|----|------|------|--------------|--------------------|
| 34 | 28 | 84.8 | 1742 | 1 MY5C_HUMAN | Q9nqx4 homo sapien |
| 35 | 28 | 84.8 | 4639 | 1 DYHC_DROME | P37276 drosophila |
| 36 | 28 | 84.8 | 4725 | 1 DYHC_DICDI | P34036 dictyosteli |
| 37 | 27 | 81.8 | 95 | 1 NCCY_ALCXX | Q44581 alcaligenes |
| 38 | 27 | 81.8 | 127 | 1 CRCB_YERPE | Q8zdh2 yersinia pe |
| 39 | 27 | 81.8 | 212 | 1 IFE4_CAEEL | Q22888 caenorhabdi |
| 40 | 27 | 81.8 | 226 | 1 ATP6_DUGDU | Q8w9n1 dugong dugo |
| 41 | 27 | 81.8 | 226 | 1 ATP6_EQUAS | P92480 equus asinu |
| 42 | 27 | 81.8 | 226 | 1 ATP6_FELCA | P48894 felis silve |
| 43 | 27 | 81.8 | 226 | 1 ATP6_HORSE | P48662 equus cabal |
| 44 | 27 | 81.8 | 311 | 1 HFLK_BORBU | O51221 borrelia bu |
| 45 | 27 | 81.8 | 340 | 1 CELF_VZVD | P09261 varicella-z |

ALIGNMENTS

| | | | | | |
|------------|---|-----------|------|---------|--|
| RESULT 1 | | | | | |
| RID2_BUCAI | | | | | |
| ID | RID2_BUCAI | STANDARD; | PRT; | 207 AA. | |
| AC | P57534; | | | | |
| DI | 28-FEB-2003 (Rel. 41, Created) | | | | |
| DI | 28-FEB-2003 (Rel. 41, Last sequence update) | | | | |
| DI | 28-FEB-2003 (Rel. 41, Last annotation update) | | | | |
| DE | 5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193) (HTP reductase). | | | | |
| DE | RIBD2 OR BU462. | | | | |
| GN | Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium). | | | | |
| OS | Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales; | | | | |
| OC | Enterobacteriaceae; Buchnera. | | | | |
| OX | NCBI_TaxID-118099; | | | | |
| RN | 111 | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=Tokyo 1998; | | | | |
| RX | MEDLINE-20445173; PubMed-10993077; | | | | |
| RA | Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.; | | | | |
| RT | "Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS." | | | | |
| RL | Nature 407:81-86(2000). | | | | |
| CC | -!- CATALYTIC ACTIVITY: 5-amino-6-(5-phosphoribitylamino)uracil + NADP(+) -> 5-amino-6-(5-phosphoribosylamino)uracil - NADPH. | | | | |
| CC | -!- PATHWAY: Riboflavin biosynthesis; third step. | | | | |
| CC | -!- SIMILARITY: BELONGS TO THE HTP REDUCTASE FAMILY. | | | | |
| CC | ----- | | | | |
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| CC | ----- | | | | |
| DR | EMBL; AP001119; BAB13159.1; -. | | | | |
| DR | InterPro; IPR002734; RibD_C. | | | | |
| DR | Pfam; PF01872; RibD_C; 1. | | | | |
| DR | TIGRFAMS; TIGR00227; ribD_Cterm; 1. | | | | |
| KW | Riboflavin biosynthesis; Oxidoreductase; NADP; Complete proteome. | | | | |
| SQ | SEQUENCE 207 AA; 23942 MW; DAC973284089D76A CRC64; | | | | |

Query Match 87.9%; Score 29; DB 1; Length 207;
Best Local Similarity 83.3%; Pred. No. 30;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
|||
Db 90 WLIRLK 95

RESULT 2
YB57_METJA
ID YB57_METJA STANDARD; PRT; 341 AA.
AC Q58558;

DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ1157.
GN MJ1157.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed-8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.L.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: BELONGS TO THE UPF0021 FAMILY.
CC
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CC
CC EMBL: U67558; AAB99161.1; -;
DR PIR: E64444; E64444.
DR TIGR: MJ1157; -;
DR InterPro: IPR000541; UPF0021.
DR Pfam: PF01171; ATP_bind3; 1.
DR TIGRFAMS: TIGR00269; TIGR00269; 1.
DR PROSITE: PS01263; UPF0021; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 341 AA; 40094 MW; B87D2AC28D5C18C3 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 341;
Best Local Similarity 83.3%; Pred. No. 50;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
| | | | |
DB 333 WLIKLK 338

RESULT 3
YBL2_SFV3L STANDARD; PRT; 388 AA.
AC P27403; Q88191;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BEL-2 protein.
GN BEL-2.
OS Simian foamy virus (type 3 / strain iK3) (SFV-3).
OC Viruses; Retroid viruses; Retroviridae; Spumavirus.
OX NCBI_TaxID=11644;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92124734; PubMed-1310187;
RA Renne R., Friedl E., Schweizer M., Fleps U., Turek R.,
RA Neumann-Haefelin D.;
RT "Genomic organization and expression of simian foamy virus type 3
(SFV-3).";
RL Virology 186:597-608(1992).

CC -!- FUNCTION: MIGHT BE IMPORTANT IN VIRAL LIFE CYCLE.
CC
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CC
CC EMBL: M74895; AAA47800.1; -;
DR EMBL: M74895; AAA47797.1; ALT_INIT.
DR InterPro: IPR004956; Foamy_BEL.
DR Pfam: PF03274; Foamy_BEL; 1.
KW Hypothetical protein.
SQ SEQUENCE 388 AA; 44527 MW; 45D6F74F3FD53966 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 388;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
| | | | |
DB 182 WLIKLK 187

RESULT 4
YJB9_YEAST STANDARD; PRT; 620 AA.
ID YJB9_YEAST
AC P47069;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 72.4 kDa protein in PET130-CCR3 intergenic region.
GN YJL019W OR J1310.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA To Van D., Perea J., Jacq C.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC
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CC
CC EMBL: Z49294; CAA89309.1; -;
DR PIR: S56790; S56790.
DR SGD: S0003556; YJL019W.
DR GO: GO:0007103; P:spindle pole body duplication (sensu Saccha. . .; IMP.
KW Hypothetical protein; Transmembrane; ATP-binding.
FT DOMAIN 88 93 POLY-ASP.
FT TRANSMEM 155 175 POTENTIAL.
FT NP_BIND 187 194 ATP (POTENTIAL).
FT DOMAIN 391 401 POLY-GLN.
SQ SEQUENCE 620 AA; 72385 MW; 18EC13469B9A5C6B CRC64;

Query Match 87.9%; Score 29; DB 1; Length 620;
Best Local Similarity 83.3%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLIQLK 6
| | | | |
DB 579 WFIQLK 584

RESULT 5

DP3A_SALTY
ID DP3A_SALTY STANDARD; PRT; 1160 AA.
AC P14567;
DT 01-JAN-1990 (Rel. 13, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase III alpha subunit (EC 2.7.7.7).
GN DNAE OR POLC OR STM0231.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90008797; PubMed-2676978;
RA Lancy E.D., Lifshits M.R., Munson P., Maurer R.;
RT "Nucleotide sequences of dnaE, the gene for the polymerase subunit of
RT DNA polymerase III in Salmonella typhimurium, and a variant that
RT facilitates growth in the absence of another polymerase subunit.";
RL J. Bacteriol. 171:5581-5586(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Lt2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed-11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
CC -!- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
CC RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
CC THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
CC THE ALPHA CHAIN IS THE DNA POLYMERASE.
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + (DNA)(N).
CC -!- SUBUNIT: DNA polymerase III contains a core (composed of alpha,
CC epsilon and theta chains) that associates with a tau subunit. This
CC core dimerizes to form the POLIII' complex. POLIII' associates
CC with the gamma complex (composed of gamma, delta, delta', psi and
CC chi chains) and with the beta chain to form the complete DNA
CC polymerase III complex. The final composition of the complex
CC is: (alpha,epsilon,theta)[2]-tau[2]-(gamma,delta,delta',
CC psi,chi)[2]-beta[4].
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-C FAMILY. DNAE
CC SUBFAMILY.
CC
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CC
CC EMBL: M29701; AAA27057.1; -.
CC EMBL: M26046; AAA27191.1; -.
CC EMBL: AE008705; AAL19195.1; -.
CC StyGene; SG10087; dnaE.
CC InterPro; IPR004013; PHP_C.
CC InterPro; IPR003141; PHP_N.
CC InterPro; IPR004805; PolC_alpha.
CC InterPro; IPR004365; trNA_anti.
CC Pfam; PF02811; PHP_C; 1.
CC Pfam; PF02231; PHP_N; 1.
CC Pfam; PF01336; trNA_anti; 1.
CC SMART; SM00481; POLIIIAC; 1.
CC TIGRFAMS; TIGR00594; polc; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW Complete proteome.

FT CONFLICT 405 405 D -> S (IN REF. 1; AAA27191).
FT CONFLICT 782 782 F -> I (IN REF. 1; AAA27191).
FT CONFLICT 997 997 A -> S (IN REF. 1; AAA27191).
FT CONFLICT 1127 1127 R -> G (IN REF. 1).
SQ SEQUENCE 1160 AA; 130217 MW; 2E9651A7C7429533 CRC64;
Query Match 87.9%; Score 29; DB 1; Length 1160;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLIQLK 6
Db 120 WLVELK 125
RESULT 6
GCSH_ORYSA STANDARD; PRT; 162 AA.
ID GCSH_ORYSA
AC O22535;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glycine cleavage system H protein, mitochondrial precursor.
GN GDCSH.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Milyang 23; TISSUE=Seed;
RA Lee M.C., Kim C.S., Eun M.Y.;
RT "Isolation and characterization of H protein from rice.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYZES THE DEGRADATION OF
CC GLYCINE. THE H PROTEIN SHUTTLES THE METHYLAMINE GROUP OF GLYCINE
CC FROM THE P PROTEIN TO THE T PROTEIN (BY SIMILARITY).
CC -!- COFACTOR: THE H CHAIN CONTAINS A COVALENTLY-BOUND LIPOYL COFACTOR
CC (BY SIMILARITY).
CC -!- SUBUNIT: The glycine cleavage system is composed of four proteins:
CC P, T, L, and H (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
CC -!- SIMILARITY: Contains 1 lipoyl-binding domain.
CC
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CC
CC EMBL: AF022731; AAB82134.1; -.
CC PIR; T02072; T02072.
CC HSSP; P16048; 1HTP.
CC Gramene; O22535; -.
CC InterPro; IPR002930; GCV_H.
CC InterPro; IPR003016; Lipoyl.
CC Pfam; PF01597; GCV_H; 1.
CC TIGRFAMS; TIGR00527; gcvH; 1.
CC PROSITE; PS00189; LIPOYL; 1.
KW Mitochondrion; Transit peptide; Lipoyl.
FT TRANSIT 1 34 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 35 162 GLYCINE CLEAVAGE SYSTEM H PROTEIN.
FT BINDING 97 97 LIPOYL (BY SIMILARITY).
SQ SEQUENCE 162 AA; 17218 MW; E212A6AE916EC0FF CRC64;
Query Match 84.8%; Score 28; DB 1; Length 162;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLIQLK 6

Db 133 WMIOVK 138
[:::]
RESULT 7
NUGC_MESVI STANDARD; PRT; 174 AA.
AC Q9MUR1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NAD(P)H-quinone oxidoreductase chain J, chloroplast (EC 1.6.5.-)
DE (NAD(P)H dehydrogenase, chain J) (NADH-plastoquinone oxidoreductase subunit J).
DE subunit J).
GN NDHJ.
OS Mesostigma viride.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae;
OC Mesostigmatales; Mesostigmataceae; Mesostigma.
OX NCBI_TaxID=41882;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-NIES-296;
RX MEDLINE=20150907; PubMed=10688199;
RA Lemieux C., Otis C., Turmel M.;
RT "Ancestral chloroplast genome in Mesostigma viride reveals an early branch of green plant evolution.";
RL Nature 403:649-652(2000).
CC -!- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P){-} + plastoquinol.
CC -!- SIMILARITY: BELONGS TO THE COMPLEX I 30 kDa SUBUNIT FAMILY.
CC -----
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CC -----
CC EMBL: AF166114; AAF43839.1; -.
DR InterPro: IPR001268; Complex1_30K.
DR Pfam: PF00329; complex1_30Kd; 1.
DR ProDom: PD001581; Complex1_30K; 1.
DR PROSITE: PS00542; Complex1_30K; 1.
KW Oxidoreductase; NAD; NADP; Quinone; Plastoquinone; Chloroplast.
SQ SEQUENCE 174 AA; 20329 MW; 122ABFA9188D47B7 CRC64;
Query Match 84.8%; Score 28; DB 1; Length 174;
Best Local Similarity 66.7%; Pred. NO. 42;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLIQLK 6
[:::]
Db 24 WLIEMK 29
[:::]
RESULT 8
GLUC_CAVPO STANDARD; PRT; 180 AA.
ID GLUC_CAVPO
AC P05110;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucagon precursor [Contains: Glucagon-related polypeptide (GRPP); Glucagon; Glucagon-37 (Oxyntomodulin); Glucagon-like peptide 1 (GLP1); Glucagon-like peptide 2 (GLP2)].
DE GCG.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=86248118; PubMed=3755107;
RA Seino S., Welsh M., Bell G.I., Chan S.J., Steiner D.F.;
RT "Mutations in the guinea pig preproglucagon gene are restricted to a specific portion of the prohormone sequence.";
RL FEBS Lett. 203:25-30(1986).
RN [2]
RP SEQUENCE OF 53-81.
RX MEDLINE=86165412; PubMed=3956884;
RA Huang C.G., Eng J., Pan Y.-C.E., Hulmes J.D., Yalow R.S.;
RT "Guinea pig glucagon differs from other mammalian glucagons.";
RL Diabetes 35:508-512(1986).
RN [3]
RP PARTIAL SEQUENCE OF 53-89.
RX MEDLINE=86017849; PubMed=4048553;
RA Conlon J.M., Hansen H.F., Schwartz T.W.;
RT "Primary structure of glucagon and a partial sequence of oxyntomodulin (glucagon-37) from the guinea pig.";
RL Regul. Pept. 11:309-320(1985).
CC -!- FUNCTION: GLUCAGON PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.
CC -!- FUNCTION: GLP2 STIMULATES INTESTINAL GROWTH AND UPREGULATES VILLUS HEIGHT IN THE SMALL INTESTINE, CONCOMITANT WITH INCREASED CRYPT CELL PROLIFERATION AND DECREASED ENTEROCYTE APOPTOSIS.
CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
CC -----
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CC -----
CC EMBL: D00014; BAA00010.1; -.
DR PIR: A24856; GCGP.
DR HSP: P01274; IGCN.
DR InterPro: IPR000532; Glucagon.
DR Pfam: PF00123; hormone2; 3.
DR PRINTS: PR00275; GLUCAGON.
DR SMART: SM00070; GLUCA; 3.
DR PROSITE: PS00260; GLUCAGON; 4.
KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20
FT PEPTIDE 21 50 GLICENTIN-RELATED POLYPEPTIDE.
FT PEPTIDE 53 81 GLUCAGON.
FT PEPTIDE 53 89 GLUCAGON-37.
FT PEPTIDE 92 128 GLUCAGON-LIKE PEPTIDE 1.
FT PROPEP 131 143
FT PEPTIDE 146 178 GLUCAGON-LIKE PEPTIDE 2.
SQ SEQUENCE 180 AA; 20972 MW; 702FB181161D2776 CRC64;
Query Match 84.8%; Score 28; DB 1; Length 180;
Best Local Similarity 83.3%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WLIQLK 6
[:::]
Db 170 WLIQTK 175
[:::]
RESULT 9
GLUC_HUMAN STANDARD; PRT; 180 AA.
ID GLUC_HUMAN
AC P01275;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Glucagon precursor [Contains: Glucagon-related polypeptide (GRPP); Glucagon; Glucagon-like peptide 1 (GLP1); Glucagon-like peptide 2 (GLP2)].

GN GCG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88330860; PubMed=2901414;
RA Drucker D.J., Asa S.;
RT "Glucagon gene expression in vertebrate brain.";
RL J. Biol. Chem. 263:13475-13478(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86259053; PubMed=3725587;
RA White J.W., Saunders G.F.;
RT "Structure of the human glucagon gene.";
RL Nucleic Acids Res. 14:4719-4730(1986).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=83271477; PubMed=6877359;
RA Bell G.I., Sanchez-Pescador R., Laybourn P.J., Najarian R.C.;
RT "Exon duplication and divergence in the human preproglucagon gene.";
RL Nature 304:368-371(1983).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.E., Dergo J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusica K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.H.,
RA Brownstein M.J., Ustin T.B., Teshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 53-81.
RA Thomsen J., Kristiansen K., Brunfeldt K., Sundby P.;
RT "The amino acid sequence of human glucagon.";
RL FEBS Lett. 21:315-319(1972).
RN [6]
RP SEQUENCE OF 98-127.
RX MEDLINE=89327238; PubMed=2753890;
RA Orskov C., Bersani M., Johnsen A.H., Hoejrup P., Holst J.J.;
RT "Complete sequences of glucagon-like peptide-1 from human and pig
small intestine.";
RL J. Biol. Chem. 264:12826-12829(1989).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 53-81.
RX MEDLINE=98334683; PubMed=9667960;
RA Sturm N.S., Lin Y., Burley S.K., Krstenansky J.L., Ahn J.M.,
RA Azizeh B.Y., Trivedi D., Hruby V.J.;
RT "Structure-function studies on positions 17, 18, and 21 replacement
analogues of glucagon: the importance of charged residues and salt
bridges in glucagon biological activity.";
RL J. Med. Chem. 41:2693-2700(1998).
CC -!- FUNCTION: GLUCAGON PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND
RAISES THE BLOOD SUGAR LEVEL.
CC -!- FUNCTION: GLP2 STIMULATES INTESTINAL GROWTH AND UPREGULATES VILLUS
HEIGHT IN THE SMALL INTESTINE, CONCOMITANT WITH INCREASED CRYPT

CC CELL PROLIFERATION AND DECREASED ENTEROCYTE APOPTOSIS.
CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
CC -!- PHARMACEUTICAL: Available under the names Glucagon (Eli Lilly) and
CC GlucaGen or Glucagon Novo Nordisk (Novo Nordisk). Used to treat
CC severe hypoglycemia in insulin-dependent diabetics.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
CC -!- DATABASE: NAME=Glucagon at Eli Lilly;
CC NOTE=Clinical information on Eli Lilly glucagon products;
CC WWW="http://www.lillydiabetes.com/products/PatientInfo.cfm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J04040; AAS52567.1; -;
CC EMBL; X03991; CAA27627.1; -;
CC EMBL; V01515; CAA24759.1; -;
CC EMBL; BC005278; AAH05278.1; -;
CC PIR; A24377; GCHU.
CC PDB; 1BH0; 18-NOV-98.
CC PDB; 1D0R; 23-OCT-02.
CC Genew; HGNC:4191; CCG.
CC MIM; 138030; -;
CC MIM; 231530; -;
CC GO; GO:0005625; C:soluble fraction; TAS.
CC GO; GO:0008283; P:cell proliferation; TAS.
CC GO; GO:0007631; P:feeding behavior; TAS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin...; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR000532; Glucagon.
CC Pfam; PF00123; hormone2; 3.
CC SMART; SM00070; GLUCA; 3.
CC PROSITE; PS00260; GLUCAGON; 4.
CC Glucagon family; Hormone; Cleavage on pair of basic residues; Signal;
CC Pharmaceutical; 3D-structure; Polymorphism.
CC SIGNAL 1 20 GLICENTIN-RELATED POLYPEPTIDE.
CC PEPTIDE 21 50 GLUCAGON.
CC PEPTIDE 53 81
CC PROPEP 84 96
CC PEPTIDE 98 127 GLUCAGON-LIKE PEPTIDE 1.
CC PROPEP 131 143 GLUCAGON-LIKE PEPTIDE 2.
CC PEPTIDE 146 178 A -> V (IN dbSNP:5650).
CC VARIANT 115 115 /FTID=VAR_014596.
CC K -> N (IN REF. 3).
CC CONFLICT 82 82
CC TURN 59 62
CC HELIX 63 77
CC TURN 78 79
CC SEQUENCE 180 AA; 20909 MW; 7A99EEC629B2862C CRC64;
SQ
Query Match 84.8%; Score 28; DB 1; Length 180;
Best Local Similarity 83.3%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WLIQLK 6
| | | | |
Db 170 WLIQTK 175
RESULT 10
GLUC_MESAU
ID GLUC_MESAU STANDARD; PRT; 180 AA.
AC P01273;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucagon precursor [Contains: Glucicentin-related polypeptide (GRPP);
DE Glucagon; Glucagon-like peptide 1 (GLP1); Glucagon-like peptide 2

DE (GLP2)].

GN GCC.

OS Mesocricetus auratus (Golden hamster).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

OC Mesocricetus.

OX NCBI_TaxID=10036;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83167563; PubMed=6835407;

RA Bell G.I., Santerre R.F., Mullenbach G.T.;

RT "Hamster proglucagon contains the sequence of glucagon and two

RT related peptides.";

RL Nature 302:716-718(1983).

RN [2]

RP REVISIONS TO 12-15.

RA Bell G.I.;

RL Submitted (XXX-1985) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: GLUCAGON PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND

CC RAISES THE BLOOD SUGAR LEVEL.

CC -!- FUNCTION: GLP2 STIMULATES INTESTINAL GROWTH AND UPREGULATES VILUS

CC HEIGHT IN THE SMALL INTESTINE, CONCOMITANT WITH INCREASED CRYPT

CC CELL PROLIFERATION AND DECREASED ENTEROCYTE APOPTOSIS.

CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS

CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.

CC -----

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CC -----

DR EMBL; J00059; AAA37074.1; -.

DR HSSP; P01274; IGCN.

DR InterPro; IPR000532; Glucagon.

DR Pfam; PF00123; hormone2; 3.

DR SMART; SM00070; GLUCA; 3.

DR PROSITE; PS00260; GLUCAGON; 4.

KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal.

FT SIGNAL 1 20 GLICENTIN-RELATED POLYPEPTIDE.

FT PEPTIDE 21 50 GLUCAGON.

FT PEPTIDE 53 81

FT PROPEP 84 89

FT PEPTIDE 92 128 GLUCAGON-LIKE PEPTIDE 1.

FT PROPEP 131 143

FT PEPTIDE 146 178 GLUCAGON-LIKE PEPTIDE 2.

SQ SEQUENCE 180 AA; 20954 MW; 02791B49D7AADD4B CRC64;

Query Match 84.8%; Score 28; DB 1; Length 180;

Best Local Similarity 83.3%; Pred. No. 44;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLIQLK 6

Db 170 WLIQTK 175

RESULT 11

GLUC_MOUSE

ID GLUC_MOUSE STANDARD; PRT; 180 AA.

AC P55095;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Glucagon precursor [Contains: Glucentin-related polypeptide (GRPP);

DE Glucagon; Glucagon-like peptide 1 (GLP1); Glucagon-like peptide 2

DE (GLP2)].

GN GCG.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX TISSUE=Pancreatic islets;

RX MEDLINE=95247722; PubMed=7730317;

RA Rothenberg M.E., Eilertson C.D., Klein K., Zhou Y., Linberg I.,

RA McDonald J.K., Mackin R.B., Noe B.D.;

RT "Processing of mouse proglucagon by recombinant prohormone convertase

RT 2 and immunopurified prohormone convertase 2 in vitro.";

RL J. Biol. Chem. 270:10136-10146(1995).

RN [2]

RP SEQUENCE FROM N.A.

RA Shamsadin R., Knepe W.;

RT "Mouse glucagon full length cDNA.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: GLUCAGON PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND

CC RAISES THE BLOOD SUGAR LEVEL.

CC -!- FUNCTION: GLP2 STIMULATES INTESTINAL GROWTH AND UPREGULATES VILUS

CC HEIGHT IN THE SMALL INTESTINE, CONCOMITANT WITH INCREASED CRYPT

CC CELL PROLIFERATION AND DECREASED ENTEROCYTE APOPTOSIS.

CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS

CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.

CC -----

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CC -----

DR EMBL; Z46845; CAA86902.1; -.

DR EMBL; AF276754; AAK96898.1; -.

DR PIR; A57294; A57294.

DR HSSP; P01274; IGCN.

DR MGD; MGI:95674; Gcg.

DR InterPro; IPR000532; Glucagon.

DR Pfam; PF00123; hormone2; 3.

DR PRINTS; PR00275; GLUCAGON.

DR SMART; SM00070; GLUCA; 3.

DR PROSITE; PS00260; GLUCAGON; 4.

KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal.

FT SIGNAL 1 20 BY SIMILARITY.

FT PEPTIDE 21 50 GLICENTIN-RELATED POLYPEPTIDE.

FT PEPTIDE 53 81 GLUCAGON.

FT PROPEP 84 89

FT PEPTIDE 92 128 GLUCAGON-LIKE PEPTIDE 1.

FT PROPEP 131 143

FT PEPTIDE 146 178 GLUCAGON-LIKE PEPTIDE 2.

SQ SEQUENCE 180 AA; 20906 MW; 595AA6DD9A589950 CRC64;

Query Match 84.8%; Score 28; DB 1; Length 180;

Best Local Similarity 83.3%; Pred. No. 44;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLIQLK 6

Db 170 WLIQTK 175

RESULT 12

GLUC_OCTDE

ID GLUC_OCTDE STANDARD; PRT; 180 AA.

AC P22890;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Glucagon precursor [Contains: Glucentin-related polypeptide (GRPP);

DE Glucagon; Glucagon-like peptide 1 (GLP1); Glucagon-like peptide 2

DE (GLP2)].

GN GCG.

```
OS Octodon degus (Dagu).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Octodontidae; Octodon.
OX NCBI_TaxID=10160;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91155952; PubMed=2293024;
RA Nishi M., Steiner D.F.;
RT "Cloning of complementary DNAs encoding islet amyloid polypeptide,
RT insulin, and glucagon precursors from a New World rodent, the degu,
RT Octodon degus.";
RL Mol. Endocrinol. 4:1192-1198(1990).
CC -!- FUNCTION: GLUCAGON PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND
CC RAISES THE BLOOD SUGAR LEVEL.
CC -!- FUNCTION: GLP2 STIMULATES INTESTINAL GROWTH AND UPREGULATES VILLUS
CC HEIGHT IN THE SMALL INTESTINE, CONCOMITANT WITH INCREASED CRYPT
CC CELL PROLIFERATION AND DECREASED ENTEROCYTE APOPTOSIS.
CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
CC -----
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CC -----
DR EMBL; M57688; AAA40588.1; -.
DR PIR; C36118; GCRTDU.
DR HSSP; P01274; IGCN.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 3.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 3.
DR PROSITE; PS00260; GLUCAGON; 4.
KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal;
KW Amidation.
FT SIGNAL 1 20
FT PEPTIDE 21 50 GLICENTIN-RELATED POLYPEPTIDE.
FT PROPEP 84 89 GLUCAGON.
FT PROPEP 92 127 GLUCAGON-LIKE PEPTIDE 1.
FT PROPEP 131 142 GLUCAGON-LIKE PEPTIDE 2.
FT PEPTIDE 146 178 AMIDATION (G-128 PROVIDE AMIDE GROUP).
FT MOD_RES 127
SQ SEQUENCE 180 AA; 21165 MW; 6E8836160A9A3051 CRC64;

Query Match 84.8%; Score 28; DB 1; Length 180;
Best Local Similarity 83.3%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLIQLK 6
DB 170 WLIQTK 175

RESULT 13
GLUC_RAT
ID GLUC_RAT STANDARD; PRT; 180 AA.
AC P06883;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucagon precursor [Contains: Glucicentin-related polypeptide (GRPP);
DE Glucagon; Glucagon-like peptide 1 (GLP1); Glucagon-like peptide 2
DE (GLP2)].
GN GCG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85054853; PubMed=6094539;
RA Heinrich G., Gros P., Habener J.F.;
RT "Glucagon gene sequence. Four of six exons encode separate functional
RT domains of rat pre-proglucagon.";
RL J. Biol. Chem. 259:14082-14087(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85051023; PubMed=6548696;
RA Heinrich G., Gros P., Lund P.K., Bentley R.C., Habener J.F.;
RT "Pre-proglucagon messenger ribonucleic acid: nucleotide and encoded
RT amino acid sequences of the rat pancreatic complementary
RT deoxyribonucleic acid.";
RL Endocrinology 115:2176-2181(1984).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86304324; PubMed=3528148;
RA Mojsov S., Heinrich G., Wilson I.B., Ravazzola M., Orci L.,
RA Habener J.F.;
RT "Preproglucagon gene expression in pancreas and intestine diversifies
RT at the level of post-translational processing.";
RL J. Biol. Chem. 261:11880-11889(1986).
CC -!- FUNCTION: GLUCAGON PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND
CC RAISES THE BLOOD SUGAR LEVEL.
CC -!- FUNCTION: GLP2 STIMULATES INTESTINAL GROWTH AND UPREGULATES VILLUS
CC HEIGHT IN THE SMALL INTESTINE, CONCOMITANT WITH INCREASED CRYPT
CC CELL PROLIFERATION AND DECREASED ENTEROCYTE APOPTOSIS.
CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
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CC -----
DR EMBL; K02813; AAA41235.1; -.
DR EMBL; K02809; AAA41235.1; JOINED.
DR EMBL; K02810; AAA41235.1; JOINED.
DR EMBL; K02811; AAA41235.1; JOINED.
DR EMBL; K02812; AAA41235.1; JOINED.
DR PIR; A22655; GCRT.
DR HSSP; P01274; IGCN.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 3.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 3.
DR PROSITE; PS00260; GLUCAGON; 4.
KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20
FT PEPTIDE 21 50 GLICENTIN-RELATED POLYPEPTIDE.
FT PROPEP 84 89 GLUCAGON.
FT PEPTIDE 92 128 GLUCAGON-LIKE PEPTIDE 1.
FT PROPEP 131 143 GLUCAGON-LIKE PEPTIDE 2.
FT PEPTIDE 146 178 GLUCAGON-LIKE PEPTIDE 2.
SQ SEQUENCE 180 AA; 20846 MW; 76931409D03C7978 CRC64;

Query Match 84.8%; Score 28; DB 1; Length 180;
Best Local Similarity 83.3%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLIQLK 6
DB 170 WLIQTK 175

RESULT 14
PURL_LACCA
```


ID AC PURL_LACCA STANDARD; PRT: 194 AA.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amidophosphoribosyltransferase precursor (EC 2.4.2.14) (Glutamine
phosphoribosylpyrophosphate amidotransferase) (ATASE) (GPATase)
(Fragment).
DE PURF.
GN Lactobacillus casei.
OS Bacteria; Firmicutes; Lactobacilliales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93012962; PubMed=1398079;
RA Gu Z.-M., Martindale D.W., Lee B.H.;
RT *Isolation and complete sequence of the purL gene encoding FGAM
synthase II in Lactobacillus casei.*;
RN Gene 119:123-126(1992).
RN [2]
RP ERRATUM.
RX MEDLINE=94040790; PubMed=8224889;
RA Gu Z.-M., Martindale D.W., Lee B.H.;
RL Gene 133:147-147(1993).
CC :- CATALYTIC ACTIVITY: 5-phospho-beta-D-ribose + diphosphate +
L-glutamate = L-glutamine + 5-phospho-alpha-D-ribose 1-diphosphate
+ H(2)O.
CC :- PATHWAY: De novo purine biosynthesis; first step.
CC :- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE
PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
CC :- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
CC -----
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CC -----
DR EMBL; M85265; AAC36948.1; -.
DR PIR; PC1136; PC1136.
DR HSSP; P00497; LA00.
DR MEROPS; C44.001; -.
DR InterPro; IPR000583; GATase_2.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR Pfam; PF00310; GATase_2; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; PARTIAL.
DR PROSITE; PS00443; GATASE_TYPE_II; 1.
KW Purine biosynthesis; Transferase; Glycosyltransferase.
FT PROPEP 1 11 BY SIMILARITY.
FT CHAIN 12 >194 AMIDOPHOSPHORIBOSYLTRANSFERASE.
FT ACT_SITE 12 12 GATASE (INVOLVED IN SUBSTRATE BINDING AND
CATALYSIS) (BY SIMILARITY).
FT NON_TER 194 194
SQ SEQUENCE 194 AA; 21144 MW; 4A788C8C5365D5EC CRC64;

Query Match 84.8%; Score 28; DB 1; Length 194;
Best Local Similarity 83.3%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLIQLK 6
Db 154 WLTQLK 159

RESULT 15
RYL2_YARLI
ID RYL2_YARLI STANDARD; PRT: 209 AA.
AC P41925;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ras-like GTP-binding protein RYL2.
GN RYL2.
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 20460 / W29;
RA Pertuiset B., Beckerich J.M., Gaillardin C.;
RL Submitted (XX-1992) to the EMBL/GenBank/DBJ databases.
CC :- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
TRAFFIC (BY SIMILARITY).
CC :- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAB FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06970; AAA35246.1; -.
DR HSSP; P36017; LEK0.
DR InterPro; IPR003579; GTPase Rab.
DR InterPro; IPR001806; Ras_trnsfrmng.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00071; Ras; 1.
DR PRINTS; PR00449; RASTRNSFRMNG.
DR SMART; SM00175; RAB; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
KW GTP-binding; Lipoprotein; Prenylation; Protein transport.
FT NP_BIND 12 19 GTP (BY SIMILARITY).
FT NP_BIND 60 64 GTP (BY SIMILARITY).
FT NP_BIND 118 121 GTP (BY SIMILARITY).
FT DOMAIN 34 42 EFFECTOR REGION (PROBABLE).
FT LIPID 208 208 GERANYL-GERANYL (BY SIMILARITY).
FT LIPID 209 209 GERANYL-GERANYL (BY SIMILARITY).
SQ SEQUENCE 209 AA; 23782 MW; 2C4697DCD084844A CRC64;

Query Match 84.8%; Score 28; DB 1; Length 209;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
Db 99 WLELEK 104

Search completed: October 14, 2003, 14:34:04
Job time : 5.41667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 ; Search time 19.875 Seconds
(without alignments)
77.903 Million cell updates/sec

Title: US-09-881-490-154
Perfect score: 33
Sequence: 1 WLIQLK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 33 | 100.0 | 136 | 16 Q8EI76 | Q8ei76 shewanella |
| 2 | 33 | 100.0 | 555 | 16 Q8G3G5 | Q8g3q5 bifidobacte |
| 3 | 33 | 100.0 | 5779 | 5 Q8IBS0 | Q8ibs0 plasmodium |
| 4 | 32 | 97.0 | 116 | 17 Q96ZA6 | Q96za6 sulfolobus |
| 5 | 32 | 97.0 | 182 | 17 Q97ZU8 | Q97zu8 sulfolobus |
| 6 | 30 | 90.9 | 1211 | 10 Q8GZF0 | Q8gzf0 glycine max |
| 7 | 29 | 87.9 | 286 | 16 Q9CMK7 | Q9cmk7 pasteurella |
| 8 | 29 | 87.9 | 287 | 16 Q98QY4 | Q98qy4 mycoplasma |
| 9 | 29 | 87.9 | 369 | 2 Q93CS6 | Q93cs6 shigella bo |
| 10 | 29 | 87.9 | 371 | 10 Q9M9K8 | Q9m9k8 arabidopsis |
| 11 | 29 | 87.9 | 390 | 3 Q42862 | Q42862 schizosacch |
| 12 | 29 | 87.9 | 415 | 10 Q9SFF6 | Q9sff6 arabidopsis |
| 13 | 29 | 87.9 | 416 | 10 Q80731 | Q80731 arabidopsis |
| 14 | 29 | 87.9 | 420 | 10 Q9M1R8 | Q9mlr8 arabidopsis |
| 15 | 29 | 87.9 | 422 | 10 Q65250 | Q65250 arabidopsis |
| 16 | 29 | 87.9 | 433 | 16 Q8G5Q6 | Q8g5q6 bifidobacte |

| | | | | | |
|----|----|------|------|-----------|--------------------|
| 17 | 29 | 87.9 | 462 | 16 Q8RIM2 | Q8rim2 fusobacteri |
| 18 | 29 | 87.9 | 756 | 10 Q9SHI4 | Q9shi4 arabidopsis |
| 19 | 29 | 87.9 | 769 | 10 Q8RVG2 | Q8rvg2 daucus caro |
| 20 | 29 | 87.9 | 819 | 5 Q9VXJ2 | Q9vxj2 drosophila |
| 21 | 29 | 87.9 | 819 | 5 Q8SXM2 | Q8sxm2 drosophila |
| 22 | 29 | 87.9 | 823 | 5 Q9NHFO | Q9nhf0 drosophila |
| 23 | 29 | 87.9 | 943 | 13 Q8JGT4 | Q8jgt4 xenopus lae |
| 24 | 29 | 87.9 | 1051 | 11 Q91XT4 | Q91xt4 mus musculu |
| 25 | 29 | 87.9 | 1058 | 11 Q92ST1 | Q92st1 rattus norv |
| 26 | 29 | 87.9 | 1160 | 16 Q829A0 | Q8z9a0 salmonella |
| 27 | 29 | 87.9 | 1195 | 10 Q8H6U5 | Q8h6u5 zea mays (m |
| 28 | 29 | 87.9 | 1208 | 10 Q8H6U8 | Q8h6u8 zea mays (m |
| 29 | 29 | 87.9 | 1222 | 10 Q8H6V1 | Q8h6v1 zea mays (m |
| 30 | 29 | 87.9 | 1222 | 10 Q8H6U6 | Q8h6u6 zea mays (m |
| 31 | 29 | 87.9 | 1226 | 10 Q8H6V0 | Q8h6v0 zea mays (m |
| 32 | 29 | 87.9 | 1247 | 10 Q8H6D9 | Q8h6d9 zea mays (m |
| 33 | 29 | 87.9 | 1251 | 10 Q8H6V3 | Q8h6v3 zea mays (m |
| 34 | 29 | 87.9 | 1251 | 10 Q8H6U7 | Q8h6u7 zea mays (m |
| 35 | 29 | 87.9 | 1251 | 10 Q8GS26 | Q8gs26 zea mays (m |
| 36 | 29 | 87.9 | 1535 | 5 Q9VPF0 | Q9vpf0 drosophila |
| 37 | 28 | 84.8 | 59 | 16 Q8YW77 | Q8yw77 anabaena sp |
| 38 | 28 | 84.8 | 62 | 16 Q9CFM6 | Q9cfm6 lactococcus |
| 39 | 28 | 84.8 | 65 | 12 Q8VAR2 | Q8var2 white spot |
| 40 | 28 | 84.8 | 66 | 9 Q38245 | Q38245 lactococcus |
| 41 | 28 | 84.8 | 108 | 8 Q9ZYN6 | Q9zyn6 caprimulgus |
| 42 | 28 | 84.8 | 146 | 16 Q9CHG1 | Q9chg1 lactococcus |
| 43 | 28 | 84.8 | 166 | 8 Q34802 | Q34802 hylobates s |
| 44 | 28 | 84.8 | 171 | 2 Q44628 | Q44628 brucella ab |
| 45 | 28 | 84.8 | 177 | 2 Q8VV80 | Q8vv80 colwellia m |

ALIGNMENTS

RESULT 1
Q8EI76
ID Q8EI76 PRELIMINARY; PRT; 136 AA.
AC Q8EI76;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN SO0971.
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MR-1;
RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
RI "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015542; AAN54045.1; -.
DR TIGR; SO0971; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 136 AA; 15529 MW; 420710910979605C CRC64;

Query Match 100.0%; Score 33; DB 16; Length 136;
Best Local Similarity 100.0%; Pred. NO. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLIQLK 6
|||||

Db 70 WLIQLK 75

RESULT 2

Q8G3G5 PRELIMINARY; PRT; 555 AA.

ID Q8G3G5

AC Q8G3G5

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Hypothetical protein.

GN BL1795

OS Bifidobacterium longum.

OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;

OC Bifidobacteriaceae; Bifidobacterium.

OX NCBI_TaxID=216816;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NCC 2705;

RX MEDLINE=22294977; PubMed=12381787;

RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,

RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Belley M.,

RA Pridmore R.D., Arigoni F.;

RT "The genome sequence of Bifidobacterium longum reflects its adaptation

RT to the human gastrointestinal tract."

RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).

DR EMBL; AE014813; AAN25578.1; -

KW Hypothetical protein; Proteasome; Complete proteome.

SQ SEQUENCE 555 AA; 61463 MW; 2B608908FE89986A CRC64;

Query Match 100.0%; Score 33; DB 16; Length 555;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6

Db 316 WLIQLK 321

RESULT 3

Q8IBSO PRELIMINARY; PRT; 5779 AA.

ID Q8IBSO

AC Q8IBSO

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Hypothetical protein.

GN MAL7P1.89.

OS Plasmodium falciparum (isolate 3D7).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=36329;

RN [1]

RP SEQUENCE FROM N.A.

RA Secger K., Murphy L., Harris D., Herriman M., Pain A., Hall N.,

RA Quail M., Bartell B.;

RL Submitted (SEP-2002) to the EMBL/GenBank/CCRB databases.

DR EMBL; AL844506; CAD50928.1; -

KW Hypothetical protein.

SQ SEQUENCE 5779 AA; 690899 MW; F930AC1A8C7B6E4C CRC64;

Query Match 100.0%; Score 33; DB 5; Length 5779;

Best Local Similarity 100.0%; Pred. No. 6.6e-02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6

Db 1529 WLIQLK 1534

RESULT 4

Q96ZA6 PRELIMINARY; PRT; 116 AA.

ID Q96ZA6

AC Q96ZA6;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Hypothetical protein ST1927.

GN ST1927.

OS Sulfolobus tokodaii.

OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;

OC Sulfolobus.

OX NCBI_TaxID=111955;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JCM 10545 / 7;

RX PubMed=11572479;

RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,

RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,

RA Oshima T., Kikuchi H.;

RT "Complete genome sequence of an aerobic thermoacidophilic

RT Crenarchaeon, Sulfolobus tokodaii strain7."

RL DNA Res. 8:123-140(2001).

DR EMBL; AP000988; BAB67020.1; -

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 116 AA; 12932 MW; 097F648F32597C42 CRC64;

Query Match 97.0%; Score 32; DB 17; Length 116;

Best Local Similarity 83.3%; Pred. No. 26;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6

Db 29 WLVQLK 34

RESULT 5

Q97ZU8 PRELIMINARY; PRT; 182 AA.

ID Q97ZU8

AC Q97ZU8;

DT 01-OCT-2001 (TrEMBLrel. 18, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)

DE Hypothetical protein SS00479.

GN SS00479.

OS Sulfolobus solfataricus.

OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;

OC Sulfolobus.

OX NCBI_TaxID=2287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 35092 / DSM 1617 / P2;

RX MEDLINE=21332296; PubMed=11427726;

RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

RA Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;

RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."

RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

DR EMBL; AE006679; AAK40800.1; -

DR InterPro; IPR000051; SAM_bind.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 182 AA; 21277 MW; E97F7EB93D725BCF CRC64;

Query Match 97.0%; Score 32; DB 17; Length 182;

Best Local Similarity 83.3%; Pred. No. 40;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6

Db 110 WLVQLK 115

```
RESULT 6
Q8GZF0 PRELIMINARY; PRT: 1211 AA.
AC Q8GZF0;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Resistance protein KR4.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Kefeng-1;
RA Wang B., Zhang J., Chen S.;
RT *Resistance gene homolog (KR4) from soybean.*;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF502080; AAC15846.1; -.
SQ SEQUENCE 1211 AA; 136972 MW; 8ABFAD93B655F6A8 CRC64;

Query Match 90.9%; Score 30; DB 10; Length 1211;
Best Local Similarity 83.3%; Pred. No. 6.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
   |||:|
Db 71 WLFQLK 76

RESULT 7
Q9CMK7 PRELIMINARY; PRT: 286 AA.
AC Q9CMK7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical protein PM0814.
GN PM0814.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurelliales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.Z., Paustian M.L., Whittam T.S., Kapur V.;
RT *Complete genomic sequence of Pasteurella multocida Pm70.*;
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006120; AAK02898.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 286 AA; 32041 MW; C0E2R335342EDC03 CRC64;

Query Match 87.9%; Score 29; DB 16; Length 286;
Best Local Similarity 83.3%; Pred. No. 2.7e-02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLIQLK 6
   || |||
Db 145 WLFQLK 150

RESULT 8
Q98QY4 PRELIMINARY; PRT: 287 AA.
AC Q98QY4;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
```

```
DE Hypothetical protein MYPU_2260.
GN MYPU_2260.
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAB CTIP;
RX MEDLINE=21267165; PubMed=11353084;
RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RL Mycoplasma pulmonis.";
RL Nucleic Acids Res. 29:2145-2153(2001).
DR EMBL; AL445563; CAC13399.1; -.
DR Mypulist; MYPU_2260; -.
DR InterPro; IPR003802; DUF199.
DR Pfam; PF02650; DUF199; 1.
DR TIGRFAMs; TIGR00647; MG103; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 287 AA; 34449 MW; DA02B90205D4BB4D CRC64;

Query Match 87.9%; Score 29; DB 16; Length 287;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
   |||:|
Db 272 WLIKLK 277

RESULT 9
Q93CS6 PRELIMINARY; PRT: 369 AA.
AC Q93CS6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative glycosyl transferase.
GN WBAT.
OS Shigella boydii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21481970; PubMed=11598067;
RA Wang L., Qu W., Reeves P.R.;
RT "Sequence Analysis of Four Shigella boydii O-Antigen Loci: Implication
RT for Escherichia coli and Shigella Relationships.";
RL Infect. Immun. 69:6923-6930(2001).
DR EMBL; AF402314; AAL27338.1; -.
DR InterPro; IPR001296; Glyco_trans_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Transferase.
SQ SEQUENCE 369 AA; 42760 MW; 3E2CCE371A6BA0BB CRC64;

Query Match 87.9%; Score 29; DB 2; Length 369;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
   |||:|
Db 361 WLIKLK 366

RESULT 10
Q9M9K8 PRELIMINARY; PRT: 371 AA.
AC Q9M9K8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
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DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Putative pectinacetylesterase.
GN F10A16.21.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC F10A16 genomic sequence.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR InterPro; IPR004963; Pec_acetylest.
DR Pfam; PF03283; PAE: 1.
SQ SEQUENCE 371 AA; 41277 MW; 7E077A8B56DA8842 CRC64;

Query Match 87.9%; Score 29; DB 10; Length 371;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
Db 88 WLIQLE 93

RESULT 11
O42862 PRELIMINARY; PRT; 390 AA.
AC O42862;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical 45.3 kDa protein.
GN SPAC25A8.02.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL021809; CAA16952.1; -;
DR GeneDB_Spombe; SPAC25A8.02; -;
KW Hypothetical protein.
SQ SEQUENCE 390 AA; 45304 MW; 203FC1DD42238F09 CRC64;

Query Match 87.9%; Score 29; DB 3; Length 390;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
Db 333 WLVQLR 338

RESULT 12
Q9SFF6 PRELIMINARY; PRT; 415 AA.
AC Q9SFF6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Putative pectinacetylesterase (At3g05910/F2010_3).
GN F2010.13 OR AT3G05910.
OS Arabidopsis thaliana (Mouse-ear cross).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC F2010 genomic sequence.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene F2010.13 (GI:6671966).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
RA Davis R.W., Ecker J.R., Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC013454; AAF23225.1; -;
DR EMBL; AF428303; AAL16135.1; -;
DR EMBL; AY050847; AAK92782.1; -;
DR EMBL; AY096751; AAM20385.1; -;
DR InterPro; IPR004963; Pec_acetylest.
DR Pfam; PF03283; PAE: 1.
SQ SEQUENCE 415 AA; 46326 MW; 4131CC9C66D35269 CRC64;

Query Match 87.9%; Score 29; DB 10; Length 415;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
Db 88 WLIQLE 93

RESULT 13
O80731 PRELIMINARY; PRT; 416 AA.
ID O80731
AC O80731;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Putative pectinesterase (At2g46930/F14M4.24).

GN AT2G4693C.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RI "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Phoeologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004411; AAC34238.1; -;
DR EMBL; AY052671; AAK96575.1; -;
DR InterPro; IPR004963; Pec_acetylest.
DR InterPro; IPR002016; Peroxidase.
DR Pfam; PF03283; PAE; 1.
DR PROSITE; PS00435; PEROXIDASE_1; -;
SQ SEQUENCE 416 AA; 45944 MW; 20D4EE2B75EEB387 CRC64;

Query Match 87.9%; Score 29; DB 10; Length 416;
Best Local Similarity 83.3%; Pred. No. 3.9e-02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
Db 89 WLIQLE 94
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89 WLIQLE 94

RESULT 14
Q9M1R8
ID Q9M1R8 PRELIMINARY; PRT; 420 AA.
AC Q9M1R8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Pectinacetylsterase precursor-like protein.
GN T17J13.20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL138651; CAB71866.1; -;
DR InterPro; IPR004963; Pec_acetylest.
DR Pfam; PF03283; PAE; 1.
SQ SEQUENCE 420 AA; 46399 MW; 42E6E8AF8A5F700A CRC64;

Query Match 87.9%; Score 29; DB 10; Length 420;
Best Local Similarity 83.3%; Pred. No. 4e-02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
Db 91 WLIQLE 96
|||||
91 WLIQLE 96

RESULT 15
O65250
ID O65250 PRELIMINARY; PRT; 422 AA.
AC O65250;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F21E10.11 protein.
GN F21E10.11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Davidson S., Rohlfing T., David M., O'Brian D.;
RT "The sequence of A. thaliana F21E10.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA WashU;
RT "The A. thaliana Genome Sequencing Project.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Waterston R.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Wilson R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF058914; AAC13595.1; -;
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR004963; Pec_acetylest.
DR Pfam; PF03283; PAE; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
SQ SEQUENCE 422 AA; 47340 MW; D9786B080A439BE4 CRC64;

Query Match 87.9%; Score 29; DB 10; Length 422;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLIQLK 6
Db 89 WLIQLE 94
|||||
89 WLIQLE 94

Search completed: October 14, 2003, 14:36:52
Job time : 21.875 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:19 ; Search time 38.625 Seconds
(without alignments)
36.985 Million cell updates/sec

Title: US-09-881-490-162
Perfect score: 48
Sequence: 1 KKWLIQLKK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 48 | 100.0 | 9 | 17 AAW04030 | Antifungal peptide |
| 2 | 48 | 100.0 | 9 | 18 AAW44559 | Anti-fungal peptid |
| 3 | 48 | 100.0 | 9 | 18 AAW44561 | Anti-fungal peptid |
| 4 | 48 | 100.0 | 9 | 18 AAW44563 | Anti-fungal peptid |
| 5 | 48 | 100.0 | 9 | 18 AAW44572 | Anti-fungal peptid |
| 6 | 48 | 100.0 | 9 | 18 AAW43753 | Bactericidal/perme |
| 7 | 48 | 100.0 | 9 | 18 AAW43749 | Bactericidal/perme |
| 8 | 48 | 100.0 | 9 | 20 AAY00536 | Antifungal peptide |
| 9 | 48 | 100.0 | 9 | 20 AAY00538 | Antifungal peptide |

| | | | | | |
|----|----|-------|----|-------------|--------------------|
| 10 | 48 | 100.0 | 9 | 20 AAY00540 | Antifungal peptide |
| 11 | 48 | 100.0 | 9 | 20 AAY00549 | Antifungal peptide |
| 12 | 48 | 100.0 | 9 | 21 AAY88384 | Antifungal peptid |
| 13 | 48 | 100.0 | 9 | 22 AAB65460 | Anti-fungal peptid |
| 14 | 48 | 100.0 | 9 | 22 AAB65462 | Anti-fungal peptid |
| 15 | 48 | 100.0 | 9 | 22 AAB65464 | Anti-fungal peptid |
| 16 | 48 | 100.0 | 9 | 22 AAB65473 | Anti-fungal peptid |
| 17 | 48 | 100.0 | 10 | 17 AAW04039 | Antifungal peptide |
| 18 | 48 | 100.0 | 10 | 17 AAW04040 | Antifungal peptide |
| 19 | 48 | 100.0 | 10 | 18 AAW44578 | Anti-fungal peptid |
| 20 | 48 | 100.0 | 10 | 18 AAW44579 | Anti-fungal peptid |
| 21 | 48 | 100.0 | 10 | 18 AAW43761 | Bactericidal/perme |
| 22 | 48 | 100.0 | 10 | 18 AAW43760 | Bactericidal/perme |
| 23 | 48 | 100.0 | 10 | 20 AAY00555 | Antifungal peptide |
| 24 | 48 | 100.0 | 10 | 20 AAY00556 | Antifungal peptide |
| 25 | 48 | 100.0 | 10 | 22 AAB65479 | Anti-fungal peptid |
| 26 | 48 | 100.0 | 10 | 22 AAB65480 | Anti-fungal peptid |
| 27 | 48 | 100.0 | 11 | 17 AAW04041 | Antifungal peptide |
| 28 | 48 | 100.0 | 11 | 18 AAW44580 | Anti-fungal peptid |
| 29 | 48 | 100.0 | 11 | 18 AAW43762 | Bactericidal/perme |
| 30 | 48 | 100.0 | 11 | 20 AAY00557 | Antifungal peptide |
| 31 | 48 | 100.0 | 11 | 22 AAB65481 | Anti-fungal peptid |
| 32 | 43 | 89.6 | 8 | 17 AAW04027 | Antifungal peptide |
| 33 | 43 | 89.6 | 8 | 17 AAW04029 | Antifungal peptide |
| 34 | 43 | 89.6 | 8 | 18 AAW44556 | Anti-fungal peptid |
| 35 | 43 | 89.6 | 8 | 18 AAW44558 | Anti-fungal peptid |
| 36 | 43 | 89.6 | 8 | 18 AAW43748 | Bactericidal/perme |
| 37 | 43 | 89.6 | 8 | 20 AAY00535 | Antifungal peptide |
| 38 | 43 | 89.6 | 8 | 20 AAY00533 | Antifungal peptide |
| 39 | 43 | 89.6 | 8 | 22 AAB65457 | Anti-fungal peptid |
| 40 | 43 | 89.6 | 8 | 22 AAB65459 | Anti-fungal peptid |
| 41 | 43 | 89.6 | 9 | 17 AAW04031 | Antifungal peptide |
| 42 | 43 | 89.6 | 9 | 17 AAW04036 | Antifungal peptide |
| 43 | 43 | 89.6 | 9 | 17 AAW04037 | Antifungal peptide |
| 44 | 43 | 89.6 | 9 | 18 AAW44564 | Anti-fungal peptid |
| 45 | 43 | 89.6 | 9 | 18 AAW44565 | Anti-fungal peptid |

ALIGNMENTS

RESULT 1

AAW04030

ID AAW04030 standard; peptide; 9 AA.

XX AAW04030;

AC AAW04030;

XX 04-NOV-1996 (first entry)

XX Antifungal peptide XMP.327/XMP.331/XMP.333/XMP.342.

KW Antifungal peptide; inhibitor; Domain III; polymorphonuclear leukocyte;
KW bactericidal/permeability-increasing protein; BPI; mammalian; PMN; fungi;
KW neutrophil; replication inhibitor; fungal infection; Aspergillus;
KW Cryptococcus; Candida; C.albicans; C.galabrat; C.krusei; C.lusitaniae;
KW C.parapsilosis; C.tropicalis; therapy.

OS Synthetic.

XX

XX

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

PF 20-JUL-1995; 95WO-US09262.
XX
PR 13-JAN-1995; 95US-0372105.
PR 15-SEP-1994; 94US-0306473.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;
XX
DR WPI; 1996-179900/18.
XX
PT Antifungal peptide(s) derived from Domain III of BPI protein - used
PT in vitro for killing or inhibiting replication of fungi, esp.
PT Candida species
XX
PS Claim 5; Page 154; 199pp; English.
XX
CC AAW04000-W04160 represent antifungal peptides. These sequences are
CC based on (or derived from) Domain III of the
CC bactericidal/permeability-increasing protein (BPI). BPI is a protein
CC that can be isolated from the granules of mammalian polymorphonuclear
CC leukocytes (PMNs or neutrophils). These antifungal peptides can be used
CC for killing, or inhibiting replication of, fungi in vitro. These
CC sequences can also be used for treatment of a fungal infection involving
CC fungi from the species Candida, Aspergillus and Cryptococcus. The
CC sequences are especially useful for treating C.albicans, C.glabrat,
CC C.krusei, C.lusitaniae, C.parapsilosis and C.tropicalis infections.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. NO. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
DQ !!!!!!!
DQ 1 KKWLQLKK 9

RESULT 2
AAW44559
ID AAW44559 standard; peptide: 9 AA.
XX
AC AAW44559;
XX
DT 27-APR-1998 (first entry)
XX
DE Anti-fungal peptide #160 based on BPI protein (residues 142-169).
XX
KW Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.
XX
OS Synthetic.
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Modified-site 9 /note= "C-terminal amide"
FT
FT
FT
XX
PN W09704008-A1.
XX
PD 06-FEB-1997.
XX
PF 21-MAR-1996; 96WO-US03845.
XX
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;
XX
DR WPI; 1997-132578/12.
XX

PT Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides
XX
PS Claim 1; Page 191; 230pp; English.
XX
CC This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. NO. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
DQ !!!!!!!
DQ 1 KKWLQLKK 9

RESULT 3
AAW44561
ID AAW44561 standard; peptide: 9 AA.
XX
AC AAW44561;
XX
DT 27-APR-1998 (first entry)
XX
DE Anti-fungal peptide #162 based on BPI protein (residues 142-169).
XX
KW Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.
XX
OS Synthetic.
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT
FT Modified-site 9 /note= "C-terminal amide"
FT
FT
XX
PN W09704008-A1.
XX
PD 06-FEB-1997.
XX
PF 21-MAR-1996; 96WO-US03845.
XX
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;
XX
DR WPI; 1997-132578/12.
XX
PT Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides
XX
PS Claim 1; Page 192; 230pp; English.
XX
CC This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in

CC decontaminating fluids and sterilising medical and implant devices.

XX Sequence 9 AA;

Query Match 100.0%; Score 48; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 4
AAW44563
ID AAW44563 standard; peptide; 9 AA.

XX AAW44563;

XX 27-APR-1998 (first entry)

DE Anti-fungal peptide #164 based on BPI protein (residues 142-169).

XX Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.

XX Synthetic.
OS Mammalia.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Modified-site 9 /note= "C-terminal amide"

FT WO9704008-A1.

XX 06-FEB-1997.

XX 21-MAR-1996; 96WO-US03845.

XX 20-JUL-1995; 95US-0504841.

XX (XOMA) XOMA CORP.

XX Fadem MB, Lim E, Little RG;

XX WPI; 1997-132578/12.

XX Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides

XX Claim 1; Page 192; 230pp; English.

XX This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.

XX Sequence 9 AA;

Query Match 100.0%; Score 48; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 5

AAW44572
ID AAW44572 standard; peptide; 9 AA.

XX AAW44572;

XX 27-APR-1998 (first entry)

DE Anti-fungal peptide #173 based on BPI protein (residues 142-169).

XX Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.

XX Synthetic.
OS Mammalia.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 8 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

XX WO9704008-A1.

XX 06-FEB-1997.

XX 21-MAR-1996; 96WO-US03845.

XX 20-JUL-1995; 95US-0504841.

XX (XOMA) XOMA CORP.

XX Fadem MB, Lim E, Little RG;

XX WPI; 1997-132578/12.

XX Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides

XX Claim 1; Page 196; 230pp; English.

XX This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.

XX Sequence 9 AA;

Query Match 100.0%; Score 48; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 6

AAW43753
ID AAW43753 standard; peptide; 9 AA.

XX AAW43753;

XX 20-APR-1998 (first entry)

XX Bactericidal/permeability increasing peptide XMP.331.
DE
XX
KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW bacterial infection; fungal infection; endotoxin; heparin;
KW angiogenesis; fungicidal; recombinant DNA; vector.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 9 /note= "Acetylated"
FT Modified-site 9 /note= "Amidated"
XX
PN W09735009-A1.
XX
PD 25-SEP-1997.
XX
PF 18-MAR-1997; 97WO-US05287.
XX
PR 22-MAR-1996; 96US-0621803.
XX
PA (XOMA) XOMA CORP.
PI Better MD;
XX
DR WPI: 1997-480215/44.
XX
PT Recombinant production of bactericidal/permeability increasing
PT protein - by expression as a fusion protein in microbial host cells,
PT then cleaving the BPI peptide from the carrier
XX
PS Claim 10; Page 127; 186pp; English.
XX
CC A new recombinant DNA vector construct has been developed which encodes
CC a fusion protein and is suitable for introduction into a bacterial host.
CC The vector comprises: (a) DNA encoding at least one cationic
CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC located between (a) and (b). The present sequence represents a
CC specifically claimed BPI peptide. The peptides have many uses including
CC the treatment of bacterial and fungal infections. BPI peptides also
CC bind to endotoxins and heparin, neutralising their effects. The
CC peptides have further been shown to inhibit angiogenesis (partly due to
CC heparin-binding activity). The fusion proteins have been found to be
CC expressed in large amounts without significant proteolysis, and in some
CC cases are actually secreted from the host cells. This allows the
CC indirect production of anti-microbial BPI peptides in microbial hosts.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9
RESULT 7
AAW43749
ID AAW43749 standard; peptide; 9 AA.
XX
AC AAW43749;
XX
DT 20-APR-1998 (first entry)
XX
DE Bactericidal/permeability increasing peptide XMP.327.
XX
KW Bactericidal/permeability increasing peptide; BPI; fusion protein;

KW bacterial infection; fungal infection; endotoxin; heparin;
KW angiogenesis; fungicidal; recombinant DNA; vector.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 9
FT Modified-site 9 /note= "Amidated"
XX
PN W09735009-A1.
XX
PD 25-SEP-1997.
XX
PF 18-MAR-1997; 97WO-US05287.
XX
PR 22-MAR-1996; 96US-0621803.
XX
PA (XOMA) XOMA CORP.
PI Better MD;
XX
DR WPI: 1997-480215/44.
XX
PT Recombinant production of bactericidal/permeability increasing
PT protein - by expression as a fusion protein in microbial host cells,
PT then cleaving the BPI peptide from the carrier
XX
PS Claim 10; Page 125; 186pp; English.
XX
CC A new recombinant DNA vector construct has been developed which encodes
CC a fusion protein and is suitable for introduction into a bacterial host.
CC The vector comprises: (a) DNA encoding at least one cationic
CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC located between (a) and (b). The present sequence represents a
CC specifically claimed BPI peptide. The peptides have many uses including
CC the treatment of bacterial and fungal infections. BPI peptides also
CC bind to endotoxins and heparin, neutralising their effects. The
CC peptides have further been shown to inhibit angiogenesis (partly due to
CC heparin-binding activity). The fusion proteins have been found to be
CC expressed in large amounts without significant proteolysis, and in some
CC cases are actually secreted from the host cells. This allows the
CC indirect production of anti-microbial BPI peptides in microbial hosts.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9
RESULT 8
AAW00536
ID AAY00536 standard; Peptide; 9 AA.
XX
AC AAY00536;
XX
DT 07-MAY-1999 (first entry)
XX
DE Antifungal peptide XMP.327.
XX
KW Antifungal; BPI; bactericidal/permeability increasing protein;
KW Candida infection.
XX
OS Synthetic.
XX
PN US5858974-A.
XX

PD 12-JAN-1999.
XX
PF 21-MAR-1996; 96US-0621259.
XX
PR 21-MAR-1996; 96US-0621259.
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;
XX
DR WPI; 1999-119956/10.
XX
PT Antifungal peptides - comprising part of bactericidal or
PT permeability-increasing protein sequence or related sequence
XX
PS Disclosure; Columns 165-166; 132pp; English.
XX
CC New peptides are provided which are based on Domain III (amino acids
CC 142-169) of human bactericidal/permeability-increasing protein (BPI).
CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGWLIQLFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, IQLF, WLIQL, LIQLF and WLIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of
CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKWLIQLKK 9
Db | | | | | | | |
1 KKWLIQLKK 9
RESULT 9
AAY00538
ID AAY00538 standard; Peptide; 9 AA.
XX
AC AAY00538;
XX
DT 07-MAY-1999 (first entry)
XX
DE Antifungal peptide XMP.331.
XX
KW Antifungal; BPI; bactericidal/permeability increasing protein;
KW Candida infection.
XX
OS Synthetic.
XX
PN US5858974-A.
XX
PD 12-JAN-1999.
XX
PF 21-MAR-1996; 96US-0621259.
XX
PR 21-MAR-1996; 96US-0621259.
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;

XX WPI; 1999-119956/10.
XX
XX Antifungal peptides - comprising part of bactericidal or
PT permeability-increasing protein sequence or related sequence
XX
PS Disclosure; Columns 165-166; 132pp; English.
XX
CC New peptides are provided which are based on Domain III (amino acids
CC 142-169) of human bactericidal/permeability-increasing protein (BPI).
CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGWLIQLFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, IQLF, WLIQL, LIQLF and WLIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of
CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKWLIQLKK 9
Db | | | | | | | |
1 KKWLIQLKK 9
RESULT 10
AAY00540
ID AAY00540 standard; Peptide; 9 AA.
XX
AC AAY00540;
XX
DT 07-MAY-1999 (first entry)
XX
DE Antifungal peptide XMP.333.
XX
KW Antifungal; BPI; bactericidal/permeability increasing protein;
KW Candida infection.
XX
OS Synthetic.
XX
PN US5858974-A.
XX
PD 12-JAN-1999.
XX
PF 21-MAR-1996; 96US-0621259.
XX
PR 21-MAR-1996; 96US-0621259.
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;
XX
DR WPI; 1999-119956/10.
XX
PT Antifungal peptides - comprising part of bactericidal or
PT permeability-increasing protein sequence or related sequence
XX
PS Disclosure; Columns 167-168; 132pp; English.
XX
CC New peptides are provided which are based on Domain III (amino acids
CC 142-169) of human bactericidal/permeability-increasing protein (BPI).

CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGLIQLFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, IQLF, WLIQL, LIQLF and WLIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of
CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLIIQLKK 9
IIIIIIII

Db 1 KKWLIIQLKK 9

RESULT 11

AA00549

ID AA00549 standard; Peptide: 9 AA.

XX
AC AA00549;

XX
07-MAY-1999 (first entry)

XX
Antifungal peptide XMP.342.

XX
Antifungal; BPI; bactericidal/permeability increasing protein;
Candida infection.

OS Synthetic.

XX
US5858974-A.

PN 12-JAN-1999.

XX
21-MAR-1996; 96US-0621259.

XX
21-MAR-1996; 96US-0621259.

PR 20-JUL-1995; 95US-0504841.

XX
(XOMA) XOMA CORP.

XX
Fadem MB, Lim E, Little RG;

PI WPI; 1999-119956/10.

XX
Antifungal peptides - comprising part of bactericidal or
permeability-increasing protein sequence or related sequence

PS Disclosure; Columns 173-174; 132pp; English.

XX
New peptides are provided which are based on Domain 1:1 (amino acids
142-169) of human bactericidal/permeability-increasing protein (BPI).

CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGLIQLFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, IQLF, WLIQL, LIQLF and WLIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of

CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLIIQLKK 9
IIIIIIII

Db 1 KKWLIIQLKK 9

RESULT 12

AA08384

ID AA08384 standard; peptide: 9 AA.

XX
AC AA08384;

XX
24-JUL-2000 (first entry)

XX
Antifungal peptide XMP.342.

XX
Antifungal peptide; XMP.342; BPI; microorganism; defence; antibacterial;
bactericidal/permeability increasing protein; antimicrobial; XMP. 445;
fungal infection; Candida; Aspergillus; Fusarium; growth inhibitor;
decontaminate; sterilize; medical equipment; prosthetic joint.

XX
Homo sapiens.

XX
Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 8 /note= "D-form residue"

FT Modified-site 9 /note= "D-form residue, C-terminal amide"

XX
WO200018798-A1.

XX
06-APR-2000.

XX
24-SEP-1999; 99WO-US22277.

XX
25-SEP-1998; 98US-0101958.

PR 25-NOV-1998; 98US-0109896.

XX
(XOMA) XOMA TECHNOLOGY LTD.

XX
Little RG;

XX
WPI; 2000-303442/26.

XX
A new antifungal peptide, designated XMP.445, used to treat fungal
infections is based on Domain III of
bactericidal/permeability-increasing protein -

XX
Example 2; Page 28; 31pp; English.

XX
This sequence represents an antifungal peptide designated XMP.342, which
is based on amino acids 153-157 of bactericidal/permeability increasing
(BPI) protein (see AAY88382). BPI is a protein isolated from the
granules of mammalian polymorphonuclear leukocytes (PMNs or neutrophils),
which are essential in the defence against invading microorganisms. BPI
protein products have antibacterial and antimicrobial activity. The
invention relates to antibacterial peptides, specifically XMP.445 (see
AAY88381). The peptide is used to treat fungal infections, particularly
infections of the species Candida, Aspergillus or Fusarium. The peptide

CC can also be used to treat a bacterial infection, or to kill or inhibit
CC the growth of bacteria in vitro. The peptide may be useful to treat
CC animals or plants in vivo, and as an agent to decontaminate fluids and
CC surfaces and to sterilize surgical or other medical equipment and
CC implantable devices including prosthetic joints.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 13
AAB65460
ID AAB65460 standard; Peptide; 9 AA.
XX
AC AAB65460;
XX
DT 27-MAR-2001 (first entry)
XX
DE Anti-fungal peptide XMP.327.
XX
KW Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;
KW bactericidal/permeability-increasing protein; bactericidal;
KW fungal infection.
XX
OS Homo sapiens.
XX
PN US6156730-A.
XX
PD 05-DEC-2000.
XX
PF 08-JAN-1999; 99US-0227659.
XX
PR 21-MAR-1996; 96US-0621259.
PR 12-MAR-1993; 93US-0030644.
PR 15-JUL-1993; 93US-0093202.
PR 14-JAN-1994; 94US-0183222.
PR 11-MAR-1994; 94US-0209762.
PR 11-JUL-1994; 94US-0273540.
PR 15-SEP-1994; 94US-0306473.
PR 13-JAN-1995; 95US-0372105.
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Lim E, Fadem MB, Little RG;
XX
DR WPI; 2001-090160/10.
XX
PT Novel anti-fungal peptides derived from domain III of
PT bactericidal/permeability-increasing protein useful for killing or
PT inhibiting replication of fungi and for treating fungal infections -
XX
PS Example 2; Columns 169-170; 134pp; English.
XX
CC The present invention relates to antifungal peptides (see
CC AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C.albicans, C.glabrata, C.krusei,
CC C.lusitanae, C.parapsilosis and C.tropicalis.
XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 14
AAB65462
ID AAB65462 standard; Peptide; 9 AA.
XX
AC AAB65462;
XX
DT 27-MAR-2001 (first entry)
XX
DE Anti-fungal peptide XMP.331.
XX
KW Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;
KW bactericidal/permeability-increasing protein; bactericidal;
KW fungal infection.
XX
OS Homo sapiens.
XX
PN US6156730-A.
XX
PD 05-DEC-2000.
XX
PF 08-JAN-1999; 99US-0227659.
XX
PR 21-MAR-1996; 96US-0621259.
PR 12-MAR-1993; 93US-0030644.
PR 15-JUL-1993; 93US-0093202.
PR 14-JAN-1994; 94US-0183222.
PR 11-MAR-1994; 94US-0209762.
PR 11-JUL-1994; 94US-0273540.
PR 15-SEP-1994; 94US-0306473.
PR 13-JAN-1995; 95US-0372105.
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Lim E, Fadem MB, Little RG;
XX
DR WPI; 2001-090160/10.
XX
PT Novel anti-fungal peptides derived from domain III of
PT bactericidal/permeability-increasing protein useful for killing or
PT inhibiting replication of fungi and for treating fungal infections -
XX
PS Example 2; Columns 171-172; 134pp; English.
XX
CC The present invention relates to antifungal peptides (see
CC AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C.albicans, C.glabrata, C.krusei,
CC C.lusitanae, C.parapsilosis and C.tropicalis.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Job time : 38.7917 secs

Qy 1 KKWLIIQLKK 9
| | | | |
Db 1 KKWLIIQLKK 9

RESULT 15
AAB65464
ID AAB65464 standard; Peptide; 9 AA.
XX
AC AAB65464:
XX
DT 27-MAR-2001 (first entry)
XX
DE Anti-fungal peptide XMP.333.
XX

KW Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;
KW bactericidal/permeability-increasing protein; bactericidal;
KW fungal infection.
XX

OS Homo sapiens.
XX
PN US6156730-A.
XX
PD 05-DEC-2000.
XX
PF 08-JAN-1999; 39US-0227659.
XX
PR 21-MAR-1996; 96US-0621259.
PR 12-MAR-1993; 93US-0030644.
PR 15-JUL-1993; 93US-0093202.
PR 14-JAN-1994; 94US-0183222.
PR 11-MAR-1994; 94US-0209762.
PR 11-JUL-1994; 94US-0273540.
PR 15-SEP-1994; 94US-0306473.
PR 13-JAN-1995; 95US-0372105.
PR 20-JUL-1995; 95US-0504841.
XX

PA (XOMA) XOMA CORP.

PI Lim E, Fadem MR, Little RG;
XX
DR WPI; 2001-090160/10.
XX

PT Novel anti-fungal peptides derived from domain III of
PT bactericidal/permeability-increasing protein useful for killing or
PT inhibiting replication of fungi and for treating fungal infections -
XX

PS Example 2; Columns 173-174; 134pp; English.
XX

CC The present invention relates to antifungal peptides (see
CC AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C.albicans, C.glabrata, C.krusei,
CC C.lusitanae, C.parapsilosis and C.tropicalis.
XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKWLIIQLKK 9
| | | | |
Db 1 KKWLIIQLKK 9

Search completed: October 14, 2003, 14:41:31

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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:23 ; Search time 12.75 Seconds
(without alignments)
29.866 Million cell updates/sec

Title: US-09-881-490-162
Perfect score: 48
Sequence: 1 KKWLIQLKK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 48 | 100.0 | 9 | 2 | US-08-621-803-193 |
| 2 | 48 | 100.0 | 9 | 2 | US-08-621-803-197 |
| 3 | 48 | 100.0 | 9 | 2 | US-08-621-259A-160 |
| 4 | 48 | 100.0 | 9 | 2 | US-08-621-259A-162 |
| 5 | 48 | 100.0 | 9 | 2 | US-08-621-259A-164 |
| 6 | 48 | 100.0 | 9 | 2 | US-08-621-259A-173 |
| 7 | 48 | 100.0 | 9 | 3 | US-09-217-352-193 |
| 8 | 48 | 100.0 | 9 | 3 | US-09-217-352-197 |
| 9 | 48 | 100.0 | 9 | 5 | PCT-US95-09262-160 |
| 10 | 48 | 100.0 | 9 | 5 | PCT-US95-09262-162 |
| 11 | 48 | 100.0 | 9 | 5 | PCT-US95-09262-164 |
| 12 | 48 | 100.0 | 9 | 5 | PCT-US95-09262-173 |
| 13 | 48 | 100.0 | 10 | 2 | US-08-621-803-204 |
| 14 | 48 | 100.0 | 10 | 2 | US-08-621-803-205 |
| 15 | 48 | 100.0 | 10 | 2 | US-08-621-259A-179 |
| 16 | 48 | 100.0 | 10 | 2 | US-08-621-259A-180 |
| 17 | 48 | 100.0 | 10 | 3 | US-09-217-352-204 |
| 18 | 48 | 100.0 | 10 | 3 | US-09-217-352-205 |
| 19 | 48 | 100.0 | 10 | 5 | PCT-US95-09262-179 |
| 20 | 48 | 100.0 | 10 | 5 | PCT-US95-09262-180 |
| 21 | 48 | 100.0 | 11 | 2 | US-08-621-803-206 |
| 22 | 48 | 100.0 | 11 | 2 | US-08-621-259A-181 |
| 23 | 48 | 100.0 | 11 | 3 | US-09-217-352-206 |
| 24 | 48 | 100.0 | 11 | 5 | PCT-US95-09262-181 |
| 25 | 43 | 89.6 | 8 | 2 | US-08-621-803-192 |
| 26 | 43 | 89.6 | 8 | 2 | US-08-621-259A-157 |
| 27 | 43 | 89.6 | 8 | 2 | US-08-621-259A-159 |

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|----|----|------|---|---|--------------------|-------------------|
| 28 | 43 | 89.6 | 8 | 3 | US-09-217-352-192 | Sequence 192, App |
| 29 | 43 | 89.6 | 8 | 5 | PCT-US95-09262-157 | Sequence 157, App |
| 30 | 43 | 89.6 | 8 | 5 | PCT-US95-09262-159 | Sequence 159, App |
| 31 | 43 | 89.6 | 9 | 2 | US-08-621-803-198 | Sequence 198, App |
| 32 | 43 | 89.6 | 9 | 2 | US-08-621-803-202 | Sequence 202, App |
| 33 | 43 | 89.6 | 9 | 2 | US-08-621-803-203 | Sequence 203, App |
| 34 | 43 | 89.6 | 9 | 2 | US-08-621-259A-165 | Sequence 165, App |
| 35 | 43 | 89.6 | 9 | 2 | US-08-621-259A-166 | Sequence 166, App |
| 36 | 43 | 89.6 | 9 | 2 | US-08-621-259A-175 | Sequence 175, App |
| 37 | 43 | 89.6 | 9 | 2 | US-08-621-259A-176 | Sequence 176, App |
| 38 | 43 | 89.6 | 9 | 2 | US-08-621-259A-206 | Sequence 206, App |
| 39 | 43 | 89.6 | 9 | 2 | US-08-621-259A-241 | Sequence 241, App |
| 40 | 43 | 89.6 | 9 | 2 | US-08-621-259A-242 | Sequence 242, App |
| 41 | 43 | 89.6 | 9 | 3 | US-09-217-352-198 | Sequence 198, App |
| 42 | 43 | 89.6 | 9 | 3 | US-09-217-352-202 | Sequence 202, App |
| 43 | 43 | 89.6 | 9 | 3 | US-09-217-352-203 | Sequence 203, App |
| 44 | 43 | 89.6 | 9 | 5 | PCT-US95-09262-165 | Sequence 165, App |
| 45 | 43 | 89.6 | 9 | 5 | PCT-US95-09262-166 | Sequence 166, App |

ALIGNMENTS

RESULT 1
US-08-621-803-193
; Sequence 193, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; FUSION PROTEINS AND BPI-DERIVED PEPTIDES
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: *XMP.327*
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= *The C-Terminus is Amidated.*
US-08-621-803-193

Query Match 100.0%; Score 48; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKWL1QLKK 9
Db 1 KKWL1QLKK 9

RESULT 2
US-08-621-803-197
; Sequence 197, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Horun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621.803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 197:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.331"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetylated
; OTHER INFORMATION: /note= "Position 1 is acetylated."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-803-197

Query Match 100.0%; Score 48; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5c+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKWL1QLKK 9
Db 1 KKWL1QLKK 9

RESULT 3
US-08-621-259A-160
; Sequence 160, Application US/08621259A
; Patent No. 5858974
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; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.327"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-160

Query Match 100.0%; Score 48; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKWL1QLKK 9
Db 1 KKWL1QLKK 9

RESULT 4
US-08-621-259A-162
; Sequence 162, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
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; 2IP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.331"
;
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetylated
; OTHER INFORMATION: /note= "Position 1 is acetylated."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
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US-08-621-259A-162

Query Match 100.0%; Score 48; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 5
US-08-621-259A-164
; Sequence 164, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; NAME: McNicholas, Janet M.
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; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.333"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= D-Lys
; OTHER INFORMATION: /note= "Position 1 is D-lysine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
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US-08-621-259A-164

Query Match 100.0%; Score 48; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 6
US-08-621-259A-173
; Sequence 173, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
```

REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11021US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX:

INFORMATION FOR SEQ ID NO: 173:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: "XMP.342"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1, 2, 8 & 9

OTHER INFORMATION: /label= D-Lys

OTHER INFORMATION: /note= "Positions 1, 2, 8 & 9 are D-lysine"

FEATURE:

NAME/KEY: Modified-site

LOCATION: C-Terminus

OTHER INFORMATION: /label= Amidation

OTHER INFORMATION: /note= "The C-Terminus is Amidated."

US-08-621-259A-173

Query Match 100.0%; Score 48; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9

|||||

DB 1 KKWLQLKK 9

RESULT 7

US-09-217-352-193

Sequence 193, Application US/09217352

Patent No. 6274344

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

TITLE OF INVENTION: Methods for Recombinant Microbial Production of

TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/217,352

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/621,803

FILING DATE: 22-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.

REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27129/33199

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 193:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.327"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-09-217-352-193

Query Match 100.0%; Score 48; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9

|||||

DB 1 KKWLQLKK 9

RESULT 8

US-09-217-352-197

Sequence 197, Application US/09217352

Patent No. 6274344

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

TITLE OF INVENTION: Methods for Recombinant Microbial Production of

TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/217,352

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/621,803

FILING DATE: 22-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.

REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27129/33199

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 197:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: "XMP.331"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /label= Acetylated

OTHER INFORMATION: /note= "Position 1 is acetylated."

FEATURE:

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; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-09-217-352-197
Query Match 100.0%; Score 48; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLIQLKK 9
Db 1 KKWLIQLKK 9

RESULT 9
PCT-US95-09262-160
; Sequence 160, Application PC/TUS9509262
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09262
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/10040
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
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; NAME/KEY: misc-feature
; OTHER INFORMATION: "XMP.327"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-160
Query Match 100.0%; Score 48; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLIQLKK 9
Db 1 KKWLIQLKK 9

RESULT 10
PCT-US95-09262-162
; Sequence 162, Application PC/TUS9509262
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09262
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/10040
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.331"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetylated
; OTHER INFORMATION: /note= "Position 1 is acetylated"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-162

Query Match 100.0%; Score 48; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 11
PCT-US95-09262-164
; Sequence 164, Application PC/TUS9509262
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09262
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25.447
; REFERENCE/DOCKET NUMBER: 27129/10040

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.333"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= D-Lys
; OTHER INFORMATION: /note= "Position 1 is D-lysine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-164

Query Match 100.0%; Score 48; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 12
PCT-US95-09262-173
; Sequence 173, Application PC/TUS9509262
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09262
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/093,202

; FILING DATE: 15-JUL-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 173:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: "XMP.342"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1, 2, 8 & 9

OTHER INFORMATION: /label= D-Lys

OTHER INFORMATION: /note= "Positions 1, 2, 8 & 9 are D-lysine"

FEATURE:

NAME/KEY: Modified-site

LOCATION: C-Terminus

OTHER INFORMATION: /label= Amidation

OTHER INFORMATION: /note= "The C-terminus is Amidated"

PCT-US95-09262-173

Query Match 100.0%; Score 48; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9

|||||

Db 1 KKWLQLKK 9

RESULT 13

US-08-621-803-204

Sequence 204, Application US/08621803

Patent No. 5851802

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

TITLE OF INVENTION: Methods for Recombinant Microbial Production of

TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/621,803

FILING DATE: 22-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.

REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27129/33199

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 204:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: "XMP.348"

FEATURE:

NAME/KEY: Modified-site

LOCATION: C-Terminus

OTHER INFORMATION: /label= Amidation

OTHER INFORMATION: /note= "The C-Terminus is Amidated."

US-08-621-803-204

Query Match 100.0%; Score 48; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.24;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9

|||||

Db 2 KKWLQLKK 10

RESULT 14

US-08-621-803-205

Sequence 205, Application US/08621803

Patent No. 5851802

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

TITLE OF INVENTION: Methods for Recombinant Microbial Production of

TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/621,803

FILING DATE: 22-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.

REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27129/33199

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 205:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: "XMP.349"

FEATURE:

NAME/KEY: Modified-site

LOCATION: C-Terminus

OTHER INFORMATION: /label= Amidation

OTHER INFORMATION: /note= "The C-Terminus is Amidated."

US-08-621-803-205

Query Match 100.0%; Score 48; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLJQLKK 9
IIIIIIII
Db 1 KKWLJQLKK 9

RESULT 15
US-08-621-259A-179
; Sequence 179, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Padem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 179:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.348"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-179

Query Match 100.0%; Score 48; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLJQLKK 9
IIIIIIII
Db 2 KKWLJQLKK 10

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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:34:14 : Search time 21.9375 Seconds
(without alignments)
66.104 Million cell updates/sec

Title: US-09-881-490-162
Perfect score: 48
Sequence: 1 KKWLIQLKK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------------------------|
| 1 | 48 | 100.0 | 9 | 9 | US-09-765-527-193 Sequence 193, App |
| 2 | 48 | 100.0 | 9 | 9 | US-09-765-527-197 Sequence 197, App |
| 3 | 48 | 100.0 | 9 | 9 | US-09-881-490-160 Sequence 160, App |
| 4 | 48 | 100.0 | 9 | 9 | US-09-881-490-162 Sequence 162, App |
| 5 | 48 | 100.0 | 9 | 9 | US-09-881-490-164 Sequence 164, App |
| 6 | 48 | 100.0 | 9 | 9 | US-09-881-490-173 Sequence 173, App |
| 7 | 48 | 100.0 | 10 | 9 | US-09-765-527-204 Sequence 204, App |
| 8 | 48 | 100.0 | 10 | 9 | US-09-765-527-205 Sequence 205, App |
| 9 | 48 | 100.0 | 10 | 9 | US-09-881-490-179 Sequence 179, App |
| 10 | 48 | 100.0 | 10 | 9 | US-09-881-490-180 Sequence 180, App |
| 11 | 48 | 100.0 | 11 | 9 | US-09-765-527-206 Sequence 206, App |
| 12 | 48 | 100.0 | 11 | 9 | US-09-881-490-181 Sequence 181, App |
| 13 | 43 | 89.6 | 8 | 9 | US-09-765-527-192 Sequence 192, App |
| 14 | 43 | 89.6 | 8 | 9 | US-09-881-490-157 Sequence 157, App |
| 15 | 43 | 89.6 | 8 | 9 | US-09-881-490-159 Sequence 159, App |

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|----|----|------|------|----|--------------------|-------------------|
| 16 | 43 | 89.6 | 9 | 9 | US-09-765-527-198 | Sequence 198, App |
| 17 | 43 | 89.6 | 9 | 9 | US-09-765-527-202 | Sequence 202, App |
| 18 | 43 | 89.6 | 9 | 9 | US-09-765-527-203 | Sequence 203, App |
| 19 | 43 | 89.6 | 9 | 9 | US-09-881-490-165 | Sequence 165, App |
| 20 | 43 | 89.6 | 9 | 9 | US-09-881-490-166 | Sequence 166, App |
| 21 | 43 | 89.6 | 9 | 9 | US-09-881-490-175 | Sequence 175, App |
| 22 | 43 | 89.6 | 9 | 9 | US-09-881-490-176 | Sequence 176, App |
| 23 | 43 | 89.6 | 10 | 9 | US-09-765-527-216 | Sequence 216, App |
| 24 | 40 | 83.3 | 10 | 9 | US-09-765-527-207 | Sequence 207, App |
| 25 | 40 | 83.3 | 10 | 9 | US-09-881-490-182 | Sequence 182, App |
| 26 | 38 | 79.2 | 7 | 9 | US-09-765-527-188 | Sequence 188, App |
| 27 | 38 | 79.2 | 7 | 9 | US-09-765-527-189 | Sequence 189, App |
| 28 | 38 | 79.2 | 7 | 9 | US-09-765-527-190 | Sequence 190, App |
| 29 | 38 | 79.2 | 7 | 9 | US-09-765-527-191 | Sequence 191, App |
| 30 | 38 | 79.2 | 7 | 9 | US-09-881-490-155 | Sequence 155, App |
| 31 | 38 | 79.2 | 7 | 9 | US-09-881-490-156 | Sequence 156, App |
| 32 | 38 | 79.2 | 7 | 9 | US-09-881-490-158 | Sequence 158, App |
| 33 | 38 | 79.2 | 9 | 9 | US-09-765-527-236 | Sequence 236, App |
| 34 | 38 | 79.2 | 9 | 9 | US-09-881-490-177 | Sequence 177, App |
| 35 | 38 | 79.2 | 10 | 9 | US-09-765-527-214 | Sequence 214, App |
| 36 | 38 | 79.2 | 11 | 9 | US-09-765-527-208 | Sequence 208, App |
| 37 | 38 | 79.2 | 11 | 9 | US-09-881-490-183 | Sequence 183, App |
| 38 | 38 | 79.2 | 11 | 9 | US-09-881-490-189 | Sequence 189, App |
| 39 | 37 | 77.1 | 10 | 9 | US-09-765-527-218 | Sequence 218, App |
| 40 | 36 | 75.0 | 9 | 9 | US-09-765-527-199 | Sequence 199, App |
| 41 | 36 | 75.0 | 9 | 9 | US-09-881-490-167 | Sequence 167, App |
| 42 | 36 | 75.0 | 436 | 10 | US-09-925-300-1640 | Sequence 1640, Ap |
| 43 | 35 | 72.9 | 55 | 11 | US-09-764-891-3233 | Sequence 3233, Ap |
| 44 | 35 | 72.9 | 2073 | 11 | US-09-978-244A-10 | Sequence 10, Appl |
| 45 | 34 | 70.8 | 9 | 9 | US-09-765-527-201 | Sequence 201, App |

ALIGNMENTS

RESULT 1

US-09-765-527-193
; Sequence 193, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids

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;
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: "XMP.327"
;   FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: C-Terminus
;   OTHER INFORMATION: /label= Amidation
;   /note= "The C-Terminus is Amidated."
;   SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-09-765-527-193
    Query Match      100.0%;   Score 48;   DB 9;   Length 9;
    Best Local Similarity 100.0%;   Pred. No. 5.4e+05;
    Matches 9;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy      1 KKWLQLKK 9
Db      1 KKWLQLKK 9

RESULT 2
US-09-765-527-197
; Sequence 197, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; City: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 197:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.331"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetylated
; /note= "Position 1 is acetylated."
; FEATURE:

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;   NAME/KEY: Modified-site
;   LOCATION: C-Terminus
;   OTHER INFORMATION: /label= Amidation
;   /note= "The C-Terminus is Amidated."
;   SEQUENCE DESCRIPTION: SEQ ID NO: 197:
US-09-765-527-197
    Query Match      100.0%;   Score 48;   DB 9;   Length 9;
    Best Local Similarity 100.0%;   Pred. No. 5.4e+05;
    Matches 9;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy      1 KKWLQLKK 9
Db      1 KKWLQLKK 9

RESULT 3
US-09-881-490-160
; Sequence 160, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; City: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/i19,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:

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; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.327"
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 160:
US-09-881-490-160

Query Match      100.0%; Score 48; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 4
US-09-881-490-162
; Sequence 162, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
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```
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.331"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetylated
; /note= "Position 1 is acetylated"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-09-881-490-162

Query Match      100.0%; Score 48; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 5
US-09-881-490-164
; Sequence 164, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
```

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.333"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= D-Lys
; /note= "Position 1 is D-lysine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-09-881-490-164

Query Match 100.0%; Score 48; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 6
US-09-881-490-173
; Sequence 173, Application US/09881490
; Patent No. US2002007298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881.490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; APPLICATION NUMBER: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94

```

```

;
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 173:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.342"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1, 2, 8 & 9
; OTHER INFORMATION: /label= D-Lys
; /note= "Positions 1, 2, 8 & 9 are D-lysine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 173:
US-09-881-490-173

Query Match 100.0%; Score 48; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 7
US-09-765-527-204
; Sequence 204, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447

```



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; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 204:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.348"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 204:
US-09-765-527-204

Query Match 100.0%; Score 48; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 2 KKWLQLKK 10

RESULT 8
US-09-765-527-205
; Sequence 205, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; MOLECULE TYPE: peptide
; FEATURE:
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; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.349"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 205:
US-09-765-527-205

Query Match 100.0%; Score 48; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 9
US-09-881-490-179
; Sequence 179, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 179:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLEFCULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.348"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 179:
US-09-881-490-179

Query Match      100.0%; Score 48; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKWLQLKK 9
      111111111
Db      2 KKWLQLKK 10

RESULT 10
US-09-881-490-180
; Sequence 180, Application US/09881490
; Patent No. US2002007298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
;           Lim, Edward
;           Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKPT NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 180:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.349"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 180:
US-09-881-490-180

Query Match      100.0%; Score 48; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKWLQLKK 9
      111111111
Db      1 KKWLQLKK 9

RESULT 11
US-09-765-527-206
; Sequence 206, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
;           Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.350"
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation

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; /note= "The C-Terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 206;
US-09-765-527-206

Query Match      100.0%; Score 48; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKWLQLKK 9
      |||||
Db      2 KKWLQLKK 10

RESULT 12
US-09-881-490-181
; Sequence 181, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
;           Lim, Edward
;           Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.350"
; FEATURE:

; /note= "The C-Terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 206;
US-09-765-527-206

Query Match      100.0%; Score 48; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKWLQLKK 9
      |||||
Db      2 KKWLQLKK 10

RESULT 13
US-09-765-527-192
; Sequence 192, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
;           Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 192:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.326"
; FEATURE:

; /note= "The C-Terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 192;
US-09-765-527-192

Query Match      89.6%; Score 43; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKWLQLK 8
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Db 1 KWLQK 8
RESULT 14
US-09-881-490-157
; Sequence 157, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 157:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.324"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 157:
US-09-881-490-157

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KWLQK 9
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Db 1 KWLQK 8
RESULT 15
US-09-881-490-159
; Sequence 159, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.326"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 159:
US-09-881-490-159

Query Match 89.68; Score 43; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKWLQLK 8
Db 1 KKWLQLK 8

Search completed: October 14, 2003, 14:44:49
Job time : 21.9375 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 ; Search time 11.6125 Seconds
(without alignments)
73.271 Million cell updates/sec

Title: US-09-881-490-162
Perfect score: 48
Sequence: 1 KKWLIIQLKK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 37 | 77.1 | 189 | AH1029 | probable membrane |
| 2 | 37 | 77.1 | 212 | T31058 | hypothetical prote |
| 3 | 37 | 77.1 | 275 | H81074 | phytoene synthase |
| 4 | 36 | 75.0 | 70 | G64500 | hypothetical prote |
| 5 | 36 | 75.0 | 89 | F91003 | Kil protein [impor |
| 6 | 36 | 75.0 | 578 | B71431 | hypothetical prote |
| 7 | 35 | 72.9 | 198 | T51962 | rac-like GTP bindi |
| 8 | 35 | 72.9 | 585 | C70341 | acetylactate synth |
| 9 | 35 | 72.9 | 731 | A99106 | hypothetical prote |
| 10 | 35 | 72.9 | 2655 | D96595 | probable acetyl-Co |
| 11 | 34 | 70.8 | 59 | AE2023 | hypothetical prote |
| 12 | 34 | 70.8 | 89 | B85638 | probable Kil prote |
| 13 | 34 | 70.8 | 89 | C95848 | hypothetical prote |
| 14 | 34 | 70.8 | 180 | T37857 | hypothetical prote |
| 15 | 34 | 70.8 | 210 | R40203 | 4-alpha-glucanotra |
| 16 | 34 | 70.8 | 276 | D81868 | probable transfera |
| 17 | 34 | 70.8 | 285 | A69748 | hypothetical prote |
| 18 | 34 | 70.8 | 287 | B90540 | conserved hypothet |
| 19 | 34 | 70.8 | 382 | S55166 | hypothetical prote |
| 20 | 34 | 70.8 | 547 | A64991 | hypothetical ABC t |
| 21 | 34 | 70.8 | 547 | D91016 | hypothetical prote |
| 22 | 34 | 70.8 | 547 | F85860 | hypothetical prote |
| 23 | 34 | 70.8 | 4588 | T28667 | dynamin beta heavy |
| 24 | 34 | 70.8 | 4639 | A54794 | dynamin heavy chain |
| 25 | 34 | 70.8 | 4725 | A44357 | dynamin heavy chain |
| 26 | 33 | 68.8 | 53 | S72388 | pd53 protein - Ent |
| 27 | 33 | 68.8 | 95 | I39575 | nickel-cobalt-cadm |
| 28 | 33 | 68.8 | 185 | D82418 | MutI/nudix family |
| 29 | 33 | 68.8 | 185 | A96989 | transcription regu |

| | | | | | | |
|----|----|------|-----|---|--------|--------------------|
| 30 | 33 | 68.8 | 201 | 2 | T48862 | rac-like protein A |
| 31 | 33 | 68.8 | 209 | 2 | T05164 | hypothetical prote |
| 32 | 33 | 68.8 | 220 | 2 | AB0084 | probable DedA-fam |
| 33 | 33 | 68.8 | 233 | 2 | D96763 | hypothetical prote |
| 34 | 33 | 68.8 | 252 | 2 | F97072 | ABC transporter, A |
| 35 | 33 | 68.8 | 264 | 2 | AE2787 | exopolysaccharide |
| 36 | 33 | 68.8 | 264 | 2 | G97566 | exopolysaccharide |
| 37 | 33 | 68.8 | 335 | 2 | A89834 | telchoic acid bios |
| 38 | 33 | 68.8 | 344 | 2 | S46871 | B13R protein - var |
| 39 | 33 | 68.8 | 344 | 2 | E72173 | D2R protein - vari |
| 40 | 33 | 68.8 | 344 | 2 | T28611 | hypothetical prote |
| 41 | 33 | 68.8 | 367 | 2 | AD3631 | nitrous-oxide redu |
| 42 | 33 | 68.8 | 396 | 2 | T46901 | hypothetical prote |
| 43 | 33 | 68.8 | 585 | 2 | A39286 | parathyroid hormon |
| 44 | 33 | 68.8 | 589 | 2 | I59297 | parathyroid hormon |
| 45 | 33 | 68.8 | 591 | 2 | S44203 | parathyroid hormon |

ALIGNMENTS

RESULT 1

AH1029
probable membrane protein STY4561 [imported] - Salmonella enterica subsp. enterica s
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 *sequence_revision 09-Nov-2001 *text_change 18-Nov-2002
C:Accession: AH1029
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churc
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Far
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A.;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica s
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH1029
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD09337.1; PID:gl6505337; GSPDB:GN00176
C:Genetics:
A:Gene: STY4561

Query Match 77.1% Score 37; DB 2; Length 189;
Best Local Similarity 66.7% Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLIIQLKK 9
|:|||||:
Db 101 KRWLIIQAKR 109

RESULT 2

T31058
hypothetical protein C05D9.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 22-Oct-1999 *sequence_revision 22-Oct-1999 *text_change 17-Mar-2000
C:Accession: T31058
R:Fulton, L.; Gattung, S.
submitted to the EMBL Data Library, September 1999
A:Description: The sequence of C. elegans cosmid C05D9.
A:Reference number: Z20960
A:Accession: T31058
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-212 <FUL>
A:Cross-references: EMBL:U64605; PIDN:AAB04584.1
A:Experimental source: strain Bristol N2
C:Genetics:
A:Map position: X
A:Introns: 21/3; 82/1; 161/2
A:Note: C05D9.5
C:Superfamily: translation initiation factor eIF-4E

Query Match 77.1%; Score 37; DB 2; Length 212;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KWLIIQLKK 9
||:|:|:|
Db 110 KWIIRLKK 117

RESULT 3
H81074
phytoene synthase-related protein NMB1521 [imported] - Neisseria meningitidis (strain MC58)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: H81074
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Venter, A.; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: H81074
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <TET>
A:Cross-references: GB:AE002501; GB:AE002098; NID:g7226755; PIDN:AAF41877.1; PID:g7226768
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1521

Query Match 77.1%; Score 37; DB 2; Length 275;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKWLIIQLKK 9
| | | | |
Db 263 KDWLMLKK 271

RESULT 4
G64500
hypothetical protein MJ1608 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: G64500
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeck, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Ison, J.D.; Sadov, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: G64500
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-70 <BUL>
A:Cross-references: GB:U67601; GB:L77117; NID:g2826439; PIDN:AAB99635.1; PID:g1500506; T
C:Genetics:
A:Map position: FOR1582918-1583130

Query Match 75.0%; Score 36; DB 2; Length 70;
Best Local Similarity 75.0%; Pred. No. 7.4;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLIIQLK 8
||:|:|
Db 63 KKWIVLKK 70

RESULT 5
F91003

kil protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C:Accession: F91003
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F91003
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-89 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA836421.1; PID:gl3362467; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
C:Superfamily: phage lambda kil protein

Query Match 75.0%; Score 36; DB 2; Length 89;
Best Local Similarity 55.6%; Pred. No. 9.3;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLIIQLKK 9
||:|:|
Db 74 KKWILMLKR 82

RESULT 6
B71431
hypothetical protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
A:Variety: Columbia
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998
C:Accession: B71431
R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; I. P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terry, N.; C. avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, E. Nature 391, 485-488, 1998
A:Authors: Mueller-Auer, S.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; C.; Chalwatzis, N.
A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis t
A:Reference number: A71400; MUID:98121113; PMID:9461215
A:Accession: B71431
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-578 <BEV>
A:Cross-references: GB:Z97341; NID:g2244991; PID:e326992; PID:g2245000
C:Genetics:
A:Map position: 4COP9-4G3845

Query Match 75.0%; Score 36; DB 2; Length 578;
Best Local Similarity 87.5%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KWLIIQLKK 9
|| | | |
Db 30 KWLIIQLKK 37

RESULT 7
T51962
Rac-like GTP binding protein [imported] - Picea mariana
C:Species: Picea mariana
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-2000
C:Accession: T51962
R:Perry, D.J.; Bousquet, J. Genetics 149, 1089-1098, 1998
A:Title: Sequence-tagged-site (STS) markers of arbitrary genes. Development, characte
A:Reference number: Z25268; MUID:98278823; PMID:9611216
A:Accession: T51962
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-198 <PER>
A:Cross-references: EMBL:AF051223; PIDN:AAC32124.1
C:Genetics:
A:Note: Sb30
C:Superfamily: ras transforming protein; translation elongation factor Tu homology

Query Match 72.9%; Score 35; DB 2; Length 198;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 8
Db 98 KKWLLELR 105

RESULT 8
C70341
acetolactate synthase (EC 4.1.3.18) large chain - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 15-Oct-1999
C:Accession: C70341
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: C70341
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-585 <AQF>
A:Cross-references: GB:AF000690; NID:g2983100; PIDN:AAC06706.1; PID:g2983101; GB:AE00069
A:Experimental source: strain VF5
C:Genetics:
A:Gene: ilvB
C:Superfamily: acetolactate synthase large chain; thiamin pyrophosphate-binding domain h
C:Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein; m
F:440-488/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 72.9%; Score 35; DB 2; Length 585;
Best Local Similarity 66.7%; Pred. No. 93;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 351 KKWLEQIEK 359

RESULT 9
A99106
hypothetical protein orf731 [imported] - Giardia theta nucleomorph
C:Species: nucleomorph Giardia theta
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: A99106
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A:Title: The highly reduced genome of an enslaved algal nucleus.
A:Reference number: A99082; MUID:11323671; PMID:11323671
A:Accession: A99106
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-731 <DOU>
A:Cross-references: GB:AJ010592; NID:gl2580677; PIDN:CAC26995.1; GSPDB:GN00151
C:Genetics:
A:Gene: orf731
A:Map position: 2
A:Genome: nucleomorph
C:Keywords: nucleomorph

Query Match 72.9%; Score 35; DB 2; Length 731;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 273 KKWLFLKK 281

RESULT 10
D96595
probable acetyl-CoA synthetase, 45051-31547 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96595
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Ali
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar
ansen, M.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Ki
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marz
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tal
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D96595
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2655 <STO>
A:Cross-references: GB:AE005173; NID:gl0645429; PIDN:AAG21546.1; GSPDB:GN00141
C:Genetics:
A:Gene: F7A10.14
A:Map position: 1

Query Match 72.9%; Score 35; DB 2; Length 2655;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 2335 KKWLQLRR 2343

RESULT 11
AE2023
hypothetical protein asl1739 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AE2023
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iri
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Taba
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacteriu
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2023
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-59 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA073438.1; PID:gl7130829; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: asl1739

Query Match 70.8%; Score 34; DB 2; Length 59;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 47 KAWLVRLKR 55

RESULT 12
B85638

```
probable kil protein of bacteriophage BP-933W kilw [imported] - Escherichia coli (strain
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C:Accession: B85638
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: B85638
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-89 <STO>
A:Cross-references: GB:AE005174; NID:gl2514292; PIDN:AAG55566.1; GSPDB:GN00145; UWGP:214
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
C:Superfamily: phage lambda kil protein

Query Match 70.8% Score 34; DB 2; Length 89;
Best Local Similarity 62.5% Pred. No. 22;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLK 8
   |||::||
Db 74 KKWLMLK 81

RESULT 13
C85848
hypothetical protein 23364 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C:Accession: C85848
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: C85848
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-89 <STO>
A:Cross-references: GB:AE005174; NID:gl2516417; PIDN:AAG57247.1; GSPDB:GN00145; UWGP:233
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z3354
C:Superfamily: phage lambda kil protein

Query Match 70.8% Score 34; DB 2; Length 89;
Best Local Similarity 62.5% Pred. No. 22;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLK 8
   |||::||
Db 74 KKWLMLK 81

RESULT 14
T37857
hypothetical protein SPAC17G8.05 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T37857
R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A:Reference number: Z21750
A:Accession: T37857
A:Status: preliminary; translated from GB/EMBL/DDRC
A:Molecule type: DNA
A:Residues: 1-180 <DEV>
A:Cross-references: EMBL:Z69795; PIDN:CAA93688.1; GSPDB:GN00066; SPDB:SPAC17G8.05
A:Experimental source: strain 972h-; cosmid cl7G8
```

C:Genetics:

A:Gene: SPDB:SPAC17G8.05
A:Map position: 1
A:Introns: 22/1

Query Match 70.8% Score 34; DB 2; Length 180;
Best Local Similarity 62.5% Pred. No. 44;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLK 8
 |||::||
Db 22 KKWVQYK 29

RESULT 15

B40203

4-alpha-glucanotransferase (EC 2.4.1.25) / amylo-1,6-glucosidase (EC 3.2.1.33) - pig
C:Species: Sus scrofa domestica (domestic pig)

C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 16-Aug-2002

C:Accession: B40203

R:Yang, B.Z.; Ding, J.H.; Enghild, J.J.; Bao, Y.; Chen, Y.T.

J. Biol. Chem. 267, 9294-9299, 1992

A:Title: Molecular cloning and nucleotide sequence of cDNA encoding human muscle gly

A:Reference number: A40203; MUID:92250533; PMID:1374391

A:Accession: B40203

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-210 <YAN>

C:Superfamily: 4-alpha-glucanotransferase / amylo-1,6-glucosidase

C:Keywords: glycosidase; glycosyltransferase; hexosyltransferase; hydrolase; polysac

Query Match 70.8% Score 34; DB 2; Length 210;

Best Local Similarity 62.5% Pred. No. 52;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKWLQLK 9

|||::||

Db 203 KWLELQK 210

Search completed: October 14, 2003, 14:38:03

Job time : 13.8125 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 ; Search time 6.375 seconds
(without alignments)
66.39i Million cell updates/sec

Title: US-09-881-490-162
Perfect score: 48
Sequence: 1 KKWLQLKK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 37 | 77.1 | 212 | 1 IFE4_CAEEL | Q22888 caenorhabdi |
| 2 | 36 | 75.0 | 70 | 1 YG08_METJA | Q59003 methanococc |
| 3 | 34 | 70.8 | 180 | 1 YD65_SCHPO | Q10317 schizosacch |
| 4 | 34 | 70.8 | 245 | 1 IFE3_HUMAN | O60573 h eukaryoti |
| 5 | 34 | 70.8 | 245 | 1 IFE3_MOUSE | Q8bmb3 mus musculu |
| 6 | 34 | 70.8 | 382 | 1 YJ07_YEAST | P47007 saccharomyc |
| 7 | 34 | 70.8 | 430 | 1 SECY_STAAU | O08387 staphylococ |
| 8 | 34 | 70.8 | 547 | 1 YOJI_ECOLI | P33941 escherichia |
| 9 | 34 | 70.8 | 4639 | 1 DYHC_DROME | P37276 drosophila |
| 10 | 34 | 70.8 | 4725 | 1 DYHC_DICDI | P34036 dictyosteli |
| 11 | 33 | 68.8 | 95 | 1 NCCY_ALCXX | Q44581 alcaligenes |
| 12 | 33 | 68.8 | 201 | 1 RAC2_ARATH | Q38903 arabidopsis |
| 13 | 33 | 68.8 | 209 | 1 V282_ARATH | O65421 arabidopsis |
| 14 | 33 | 68.8 | 218 | 1 GCH1_PASMU | P57865 pasteurella |
| 15 | 33 | 68.8 | 267 | 1 EXOR_RHILV | Q52822 rhizobium l |
| 16 | 33 | 68.8 | 344 | 1 SPI2_VARV | P33830 variola vir |
| 17 | 33 | 68.8 | 396 | 1 PTD4_HUMAN | Q9ntk5 homo sapien |
| 18 | 33 | 68.8 | 396 | 1 PTD4_MOUSE | Q9cz30 mus musculu |
| 19 | 33 | 68.8 | 585 | 1 PTRR_DIDMA | P25107 didelphis m |
| 20 | 33 | 68.8 | 585 | 1 PTRR_PIG | P50133 sus scrofa |
| 21 | 33 | 68.8 | 591 | 1 PTRR_MOUSE | P41593 mus musculu |
| 22 | 33 | 68.8 | 591 | 1 PTRR_RAT | P25962 rattus norv |
| 23 | 33 | 68.8 | 593 | 1 PTRR_HUMAN | Q03431 homo sapien |
| 24 | 33 | 68.8 | 639 | 1 NOS2_RHIME | Q59746 rhizobium m |
| 25 | 33 | 68.8 | 650 | 1 MT10_CAEEL | P34400 caenorhabdi |
| 26 | 33 | 68.8 | 1742 | 1 MY5C_HUMAN | Q9cqx4 homo sapien |
| 27 | 33 | 68.8 | 1877 | 1 PKK5_MOUSE | Q04592 mus musculu |
| 28 | 33 | 68.8 | 2109 | 1 RRPL_VSVJH | P13615 vesicular s |
| 29 | 32 | 66.7 | 290 | 1 Y084_MYCGE | P47330 mycoplasma |
| 30 | 32 | 66.7 | 387 | 1 HODG_MOUSE | Q924y0 mus musculu |
| 31 | 32 | 66.7 | 387 | 1 HODG_RAT | Q9qzu7 rattus norv |
| 32 | 32 | 66.7 | 423 | 1 AATM_CHICK | P00508 gallus gall |
| 33 | 32 | 66.7 | 454 | 1 Y095_MYCPN | P75538 mycoplasma |

ALIGNMENTS

RESULT 1

| IFE4_CAEEL | ID | IFE4_CAEEL | STANDARD | PRT | 212 AA |
|------------|--|------------|----------|-----|--------|
| AC | Q22888; | | | | |
| DI | 01-NOV-1997 (Rel. 35, Created) | | | | |
| DI | 01-NOV-1997 (Rel. 35, Last sequence update) | | | | |
| DI | 28-FEB-2003 (Rel. 41, Last annotation update) | | | | |
| DE | Eukaryotic translation initiation factor 4E (eIF-4E) (mRNA | | | | |
| DE | cap-binding protein) (eIF-4F 25 kDa subunit). | | | | |
| GN | IFE-4 OR C05D9.5. | | | | |
| OS | Caenorhabditis elegans. | | | | |
| OC | Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; | | | | |
| OC | Rhabditidae; Peloderinae; Caenorhabditis. | | | | |
| OX | NCBI_TaxID=6239; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=Bristol N2; | | | | |
| RX | MEDLINE=20209441; PubMed=10744754; | | | | |
| RA | Keiper B.D., Lamphear B.J., Deshpande A.M., Jankowska-Anyszka M., | | | | |
| RA | Aamodt E.J., Blumenthal T., Rhoads R.E.; | | | | |
| RT | *Functional characterization of five eIF4E isoforms in Caenorhabditis | | | | |
| RT | elegans."; | | | | |
| RL | J. Biol. Chem. 275:10590-10596(2000). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=Bristol N2; | | | | |
| RA | Fulton L., Gattung S.; | | | | |
| RL | Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases. | | | | |
| CC | !- FUNCTION: RECOGNIZES AND BINDS THE 7-METHYLGUANOSINE-CONTAINING | | | | |
| CC | MRNA "CAP" DURING AN EARLY STEP IN THE INITIATION OF PROTEIN | | | | |
| CC | SYNTHESIS AND FACILITATES RIBOSOME BINDING BY INDUCING THE | | | | |
| CC | UNWINDING OF THE MRNAS SECONDARY STRUCTURES. | | | | |
| CC | !- SUBUNIT: EIF4F IS A TRIMER COMPOSED OF EIF4E, EIF4G AND EIF4A | | | | |
| CC | (WHICH CAN CYCLE IN AND OUT OF THE COMPLEX). | | | | |
| CC | !- SIMILARITY: BELONGS TO THE EUKARYOTIC INITIATION FACTOR 4E FAMILY. | | | | |
| CC | ----- | | | | |
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| CC | entities requires a license agreement (See http://www.isb-sib.ch/announce/ | | | | |
| CC | or send an email to license@isb-sib.ch). | | | | |
| CC | ----- | | | | |
| DR | EMBL; AF214651; AAF62414.1; -. | | | | |
| DR | EMBL; U64605; AAF98601.1; -. | | | | |
| DR | PIR; T31058; T31058. | | | | |
| DR | HSSP; P07260; IAP8. | | | | |
| DR | WormPep; C05D9.5; CE07931. | | | | |
| DR | InterPro; IPR001040; TIF_eIF_4E. | | | | |
| DR | Pfam; PF01652; IF4E; 1. | | | | |
| DR | ProDom; PD003697; TIF_eIF_4E; 1. | | | | |
| DR | PROSITE; PS00813; IF4E; 1. | | | | |
| KW | Initiation factor; Protein biosynthesis; RNA-binding; | | | | |
| KW | Multigene family. | | | | |
| SQ | SEQUENCE 212 AA; 24584 MW; 87BA3DFE9FE8A486 CRC64; | | | | |

Q01926 saccharomyc
P44985 haemophilus
Q8xbh3 clostridium
P10978 nicotiana t
P41832 saccharomyc
P03758 bacterioph
Q58551 methanococc
O82198 arabidopsis
P20002 sus scrofa
P19596 gallus gall
P05230 homo sapien
P34004 mesocricetu

34 32 66.7 470 1 MRS2_YEAST
35 32 66.7 538 1 THIP_HAEIN
36 32 66.7 1067 1 CARB_CLOPE
37 32 66.7 1328 1 POLX_TOBAC
38 31.5 65.6 1953 1 BNIL_YEAST
39 31 64.6 89 1 VKIL_LAMBD
40 31 64.6 113 1 YB51_METJA
41 31 64.6 124 1 LBD9_ARATH
42 31 64.6 152 1 FGF1_PIG
43 31 64.6 155 1 FGF1_CHICK
44 31 64.6 155 1 FGF1_HUMAN
45 31 64.6 155 1 FGF1_MESAU

Query Match 77.1%; Score 37; DB 1; Length 212;
Best Local Similarity 75.0%; Pred. No. 5.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KWLQLKK 9
Db 110 KWIIRLKK 117

RESULT 2

YG08_METJA STANDARD; PRT; 70 AA.
AC Q59003;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ1608.
GN MJ1608.

OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT *Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.*;
RL Science 273:1058-1073(1996).

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CC or send an email to license@isb-sib.ch).

DR EMBL; U67601; AAB99635.1; -
DR PIR; G64500; G64500.
DR TIGR; MJ1608; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 70 AA; 8122 MW; BDC6BESALA47AF57 CRC64;

Query Match 75.0%; Score 36; DB 1; Length 70;
Best Local Similarity 75.0%; Pred. No. 2.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLIQLK 8
Db 63 KKWIKLK 70

RESULT 3

YD65_SCHPO STANDARD; PRT; 180 AA.
AC Q10317;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein Cl7G8.05 in chromosome I.
GN SPAC17G8.05.

OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor K., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT *The genome sequence of Schizosaccharomyces pombe.*;
RL Nature 415:871-880(2002).

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DR EMBL; Z69795; CAA93688.1; -
DR PIR; T37857; T37857.
DR GeneDB_SPombe; SPAC17G8.05; -
KW Hypothetical protein.
SQ SEQUENCE 180 AA; 20931 MW; A471D5243297E0B2 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 180;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLIQLK 8
Db 22 KKWVVQYK 29

RESULT 4

IFE3_HUMAN STANDARD; PRT; 245 AA.
AC O60573; O75349;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Eukaryotic translation initiation factor 4E type 3 (eIF-4E type 3)
DE (eIF4E type 3) (mRNA cap-binding protein type 3) (Eukaryotic
DE translation initiation factor 4E-like 3) (Eukaryotic translation
DE initiation factor 4E homologous protein) (mRNA cap-binding protein
DE 4EHP) (eIF4E-like protein 4E-LP).
GN EIF4EL3.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., CHARACTERIZATION, 3D-STRUCTURE MODELING, AND
RP MUTAGENESIS.
RC TISSUE=Pollicle;
RX MEDLINE=98250763; PubMed=9582349;
RA Rom E., Kim H.C., Gingras A.-C., Marcotrigiano J., Favre D., Olsen H.,
RA Burley S.K., Sonenberg N.;
RT "Cloning and characterization of 4EHP, a novel mammalian eIF4E-related
RT cap-binding protein.";
RL J. Biol. Chem. 273:13104-13109(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RA Joshi B., Norris K.K., Jagus R.;
RT "Isolation of human and mouse cDNAs encoding novel eIF4E-like
RT proteins.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=98318631; PubMed=9653160;
RA Mao M., Fu G., Wu J.-S., Zhang Q.-H., Zhou J., Kan L.-X., Huang Q.-H.,
RA He K.-L., Gu B.-W., Han Z.-G., Shen Y., Gu J., Yu Y.-P., Xu S.-H.,
RA Wang Y.-X., Chen S.-J., Chen Z.;
RT "Identification of genes expressed in human CD34(+) hematopoietic
RT stem/progenitor cells by expressed sequence tags and efficient full-
RT length cDNA cloning.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8175-8180(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle, Urinary bladder, and Uterus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore I., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Recognizes and binds the 7-methylguanosine-containing
CC mRNA "CAP" during an early step in the initiation of protein
CC synthesis and facilitates ribosome binding by inducing the
CC unwinding of the mRNAs secondary structures.
CC -!- SUBUNIT: EIF4F is a trimer composed of EIF4E, EIF4G and EIF4A
CC (which can cycle in and out of the complex) (By similarity).
CC -!- SIMILARITY: BELONGS TO THE EUKARYOTIC INITIATION FACTOR 4E FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF047695; AAC18565.1; -;
DR EMBL: AF068117; AAC19374.1; -;
DR EMBL: AF038957; AAC39871.1; -;
DR EMBL: BC005392; AAH05392.1; -;

DR EMBL: BC005874; AAH05874.1; -;
DR EMBL: BC021226; AAH21226.1; -;
DR EMBL: BC021690; AAH21690.1; -;
DR Genew; HGNC:3293; EIF4EL3.
DR MIM; 605895; -;
DR GO; GO:0003731; F:mrna cap binding; TAS.
DR GO; GO:0006445; P:regulation of translation; TAS.
DR InterPro; IPR01040; TIF_eIF_4E.
DR Pfam; PF01652; IF4E; 1.
DR ProDom; PD003697; TIF_eIF_4E; 1.
DR PROSITE; PS00813; IF4E; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding;
KW Multigene family.
FT MUTAGEN 63 63 W->A: UNABLE TO BIND CAPPED RNA.
FT MUTAGEN 95 95 W->A: ABILITY TO BIND CAPPED MRNA REDUCED
FT TO 40% OF WILD-TYPE.
FT MUTAGEN 124 126 WED->FAA: UNABLE TO BIND CAPPED RNA.
FT MUTAGEN 124 124 W->A: ABILITY TO BIND CAPPED MRNA REDUCED
FT TO LESS THAN 10% OF WILD-TYPE.
FT MUTAGEN 124 124 W->F: ABILITY TO BIND CAPPED MRNA REDUCED
FT TO 13% OF WILD-TYPE.
FT MUTAGEN 125 125 E->A: ABILITY TO BIND CAPPED MRNA REDUCED
FT TO LESS THAN 10% OF WILD-TYPE.
FT MUTAGEN 126 126 D->A: SLIGHT REDUCTION IN ABILITY TO BIND
FT CAPPED RNA.
FT MUTAGEN 135 135 W->A: UNABLE TO BIND CAPPED RNA.
FT MUTAGEN 148 148 W->A: UNABLE TO BIND CAPPED RNA.
FT MUTAGEN 183 183 W->A: ABILITY TO BIND CAPPED MRNA REDUCED
FT TO LESS THAN 10% OF WILD-TYPE.
FT MUTAGEN 183 183 W->F: UNABLE TO BIND CAPPED RNA.
FT CONFLICT 1 27 MNKEDALKDDSDGHDQNEENSTQKD -> MMTVGTMTIRM
FT KKTARHKI (IN REF. 3).
SQ SEQUENCE 245 AA; 28362 MW; 3D3075BFA48B3C12 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 245;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 KWLQLKK 9
||:|:|:
DB 134 KWIIRLK 141

RESULT 5
IFE3_MOUSE STANDARD; PRT; 245 AA.
AC Q8BMB3; O88503;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Eukaryotic translation initiation factor 4E type 3 (eIF-4E type 3)
DE (eIF4E type 3) (mRNA cap-binding protein type 3) (Eukaryotic
DE translation initiation factor 4E-like 3) (eIF4E-like protein 4E-LP).
GN EIF4EL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH Swiss;
RA Joshi B., Jagus R.;
RT "Isolation of human and mouse cDNAs encoding novel eIF4E-like
RT proteins.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,


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DR PRINTS; PR00303; SPCYTRNLCASE.
DR TIGRFAMS; TIGR00967; 3a0501s007; 1.
DR PROSITE; PS00755; SECY_1; 1.
DR PROSITE; PS00756; SECY_2; 1.
KW Protein transport; Translocation; Transmembrane.
SQ SEQUENCE 430 AA; 47612 MW; AF6923FE32434031 CRC64;

Query Match          70.8%; Score 34; DB 1; Length 430;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLK 8
DB 333 KKWLITL 340

RESULT 8
YOJI_ECOLI
ID YOJI_ECOLI STANDARD; PRT; 547 AA.
AC P33941; P33942;
DT 01-FEB-1994 (Rel. 28, Created)
DI 01-JUN-1994 (Rel. 29, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical ABC transporter ATP-binding protein yoji.
GN YOJI OR B2211.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / BHB2600;
RA Richterich P., Lakey N., Gryan G., Jaehn L., Mintz L., Robison K.,
RA Church G.M.;
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampei G., Seki Y., Sivasubram S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi I.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. SIMILAR TO
CC P.SYRINGAE SYRD.
CC
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CC -----
DR EMBL; U00008; AAA16403.1; -.
DR EMBL; AF000310; AAC75271.1; -.
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DR EMBL; D90850; BAA15994.1; -.
DR PIR; A64991; A64991.
DR EcoGene; EG12070; yoj1.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABC_TM_transpt.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR005898; Cyc_pep_transpt.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMS; TIGR01194; cyc_pep_trnspt; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW Hypothetical protein; ATP-binding; Transport; Transmembrane;
KW Inner membrane; Complete proteome.
FT TRANSMEM 16 36 POTENTIAL.
FT TRANSMEM 48 68 POTENTIAL.
FT TRANSMEM 125 145 POTENTIAL.
FT TRANSMEM 149 169 POTENTIAL.
FT TRANSMEM 240 260 POTENTIAL.
FT TRANSMEM 270 290 POTENTIAL.
FT NP_BIND 356 363 ATP (POTENTIAL).
SQ SEQUENCE 547 AA; 61552 MW; 11523935EDFD9EAB CRC64;

Query Match          70.8%; Score 34; DB 1; Length 547;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLK 8
DB 426 EKWLQLK 433

RESULT 9
DYHC_DROME
ID DYHC_DROME STANDARD; PRT; 4639 AA.
AC P37276;
DI 01-OCT-1994 (Rel. 30, Created)
DI 01-OCT-1994 (Rel. 30, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dynein heavy chain, cytosolic (DYHC).
GN CDHC OR DHC64C.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94375524; PubMed=8089180;
RA Li M., McGrail M., Serr M., Hays T.S.;
RT "Drosophila cytoplasmic dynein, a microtubule motor that is
RT asymmetrically localized in the oocyte.";
RL J. Cell Biol. 126:1475-1494(1994).
RN [2]
RP SEQUENCE OF 1877-1998 FROM N.A.
RX MEDLINE=94243034; PubMed=8186464;
RA Rasmusson K., Serr M., Gepner J., Gibbons I., Hays T.S.;
RT "A family of dynein genes in Drosophila melanogaster.";
RL Mol. Biol. Cell 5:45-55(1994).
CC -!- FUNCTION: Cytoplasmic dynein acts as a motor for the intracellular
CC retrograde motility of vesicles and organelles along microtubules.
CC Dynein has ATPase activity; the force-producing power stroke is
CC thought to occur on release of ADP.
CC -!- SUBUNIT: Consists of at least two heavy chains and a number of
CC intermediate and light chains.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem
CC (which binds cargo and interacts with other dynein components),
CC and the head or motor domain. The motor contains six tandemly-
CC linked AAA domains in the head, which form a ring. A stalk-like
CC structure (formed by two of the coiled coil domains) protrudes
```


between AAA 4 and AAA 5 and terminates in a microtubule-binding site. A seventh domain may also contribute to this ring; it is not clear whether the N-terminus or the C-terminus forms this extra domain. There are four well-conserved and two non-conserved ATPase sites, one per AAA domain. Probably only one of these (within AAA 1) actually hydrolyzes ATP, the others may serve a regulatory function.

!- SIMILARITY: Belongs to the dynein heavy chain family.

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EMBL; L23195; AAA60323.1; -
 EMBL; L25122; AAA28492.1; -
 PIR; A54794; A54794.
 FlyBase: FBgn0010349; Dhc64C.
 GO; GO:0045169; C:fusome; NAS.
 GO; GO:0008567; F:dynein ATPase motor activity; IDA.
 GO; GO:0003777; F:microtubule motor activity; IDA.
 GO; GO:0007098; P:centrosome cycle; IMP.
 GO; GO:0045478; P:fusome organization and biogenesis; NAS.
 GO; GO:0007018; P:microtubule-based movement; IDA.
 GO; GO:0007294; P:oocyte determination; IMP.
 GO; GO:0007292; P:oogenesis; IMP.
 InterPro; IPR003593; AAA_ATPase.
 InterPro; IPR004273; Dynein_heavy.
 Pfam; PF03028; Dynein_heavy; 1.
 SMART; SM00382; AAA; 4.
 Motor protein; Dynein; Microtubules; ATP-binding; Repeat; Coiled coil.

FT DOMAIN 1 1856 STEM (BY SIMILARITY).
 FT DOMAIN 1857 2084 AAA 1 (BY SIMILARITY).
 FT DOMAIN 2166 2437 AAA 2 (BY SIMILARITY).
 FT DOMAIN 2541 2790 AAA 3 (BY SIMILARITY).
 FT DOMAIN 2884 3153 AAA 4 (BY SIMILARITY).
 FT DOMAIN 3189 3478 STALK (BY SIMILARITY).
 FT DOMAIN 3539 3768 AAA 5 (BY SIMILARITY).
 FT DOMAIN 3989 4205 AAA 6 (BY SIMILARITY).
 FT DOMAIN 530 565 COILED COIL (POTENTIAL).
 FT DOMAIN 774 794 COILED COIL (POTENTIAL).
 FT DOMAIN 1264 1368 COILED COIL (POTENTIAL).
 FT DOMAIN 3189 3261 COILED COIL (POTENTIAL).
 FT DOMAIN 3382 3478 COILED COIL (POTENTIAL).
 FT DOMAIN 3723 3782 COILED COIL (POTENTIAL).
 FT NP_BIND 1895 1902 ATP (POTENTIAL).
 FT NP_BIND 2210 2217 ATP (POTENTIAL).
 FT NP_BIND 2580 2587 ATP (POTENTIAL).
 FT NP_BIND 2922 2929 ATP (POTENTIAL).
 SQ SEQUENCE 4639 AA; 530152 MW; 057A7D8800CCD07E CRC64;

Query Match 70.8%; Score 34; DB 1; Length 4639;
 Best Local Similarity 62.5%; Pred. No. 3.8e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 KWLQLKK 9
 :||:|:|:
 Db 4088 QWLVLQLEK 4095

RESULT 10
 DYHC_DICDI STANDARD; PRT; 4725 AA.
 AC P34036;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Dynein heavy chain, cytosolic (DYHC).
 GN DHCA.
 OS Dictyostelium discoideum (Slime mold).

Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 NCBI_TaxID=44689;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN=AX3;
 RX MEDLINE=93107159; PubMed=1469051;
 RA Koonce M.P., Grissom P.M., McIntosh J.R.;
 RT "Dynein from Dictyostelium: primary structure comparisons between a cytoplasmic motor enzyme and flagellar dynein.";
 RL J. Cell Biol. 119:1597-1604(1992).
 [2]
 CHARACTERIZATION.
 MEDLINE=95170719; PubMed=7866389;
 RA Koonce M.P., Grissom P.M., Lyon M., Pope T., McIntosh J.R.;
 RT "Molecular characterization of a cytoplasmic dynein from Dictyostelium.";
 RL J. Eukaryot. Microbiol. 41:645-651(1994).
 CC !- FUNCTION: Cytoplasmic dynein acts as a motor for the intracellular retrograde motility of vesicles and organelles along microtubules. Dynein has ATPase activity; the force-producing power stroke is thought to occur on release of ADP.
 CC !- SUBUNIT: Consists of at least two heavy chains and a number of intermediate and light chains.
 CC !- SUBCELLULAR LOCATION: Cytoplasmic.
 CC !- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem (which binds cargo and interacts with other dynein components), and the head or motor domain. The motor contains six tandemly-linked AAA domains in the head, which form a ring. A stalk-like structure (formed by two of the coiled coil domains) protrudes between AAA 4 and AAA 5 and terminates in a microtubule-binding site. A seventh domain may also contribute to this ring; it is not clear whether the N-terminus or the C-terminus forms this extra domain. There are four well-conserved and two non-conserved ATPase sites, one per AAA domain. Probably only one of these (within AAA 1) actually hydrolyzes ATP, the others may serve a regulatory function.

!- SIMILARITY: Belongs to the dynein heavy chain family.

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EMBL; Z15124; CAA78827.1; -
 PIR; A44357; A44357.
 DictyDb; DD01045; dhca.
 InterPro; IPR003593; AAA_ATPase.
 InterPro; IPR004273; Dynein_heavy.
 Pfam; PF03028; Dynein_heavy; 1.
 SMART; SM00382; AAA; 3.
 Motor protein; Dynein; Microtubules; ATP-binding; Repeat; Coiled coil.

FT DOMAIN 1 1930 STEM (BY SIMILARITY).
 FT DOMAIN 1931 2153 AAA 1 (BY SIMILARITY).
 FT DOMAIN 2233 2526 AAA 2 (BY SIMILARITY).
 FT DOMAIN 2630 2880 AAA 3 (BY SIMILARITY).
 FT DOMAIN 2973 3247 AAA 4 (BY SIMILARITY).
 FT DOMAIN 3266 3580 STALK (BY SIMILARITY).
 FT DOMAIN 3633 3862 AAA 5 (BY SIMILARITY).
 FT DOMAIN 4093 4307 AAA 6 (BY SIMILARITY).
 FT DOMAIN 864 897 COILED COIL (POTENTIAL).
 FT DOMAIN 1199 1219 COILED COIL (POTENTIAL).
 FT DOMAIN 1338 1367 COILED COIL (POTENTIAL).
 FT DOMAIN 1420 1436 COILED COIL (POTENTIAL).
 FT DOMAIN 1656 1684 COILED COIL (POTENTIAL).
 FT DOMAIN 2226 2248 COILED COIL (POTENTIAL).
 FT DOMAIN 2437 2457 COILED COIL (POTENTIAL).
 FT DOMAIN 3266 3344 COILED COIL (POTENTIAL).
 FT DOMAIN 3478 3580 COILED COIL (POTENTIAL).
 FT DOMAIN 3849 3876 COILED COIL (POTENTIAL).
 FT NP_BIND 1969 1976 ATP (POTENTIAL).


```
FT NP_BIND 2271 2278 ATP (POTENTIAL).
FT NP_BIND 2669 2676 ATP (POTENTIAL).
FT NP_BIND 3011 3018 ATP (POTENTIAL).
SQ SEQUENCE 4725 AA; 538807 MW; 9A0319915D579D3A CRC64;

Query Match 70.8%; Score 34; DB 1; Length 4725;
Best Local Similarity 62.5%; Pred. No. 3.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 KWLQLKK 9
Db 4190 QWLVLQLEK 4197

RESULT 11
NCCY_ALCXX STANDARD; PRT; 95 AA.
AC Q44581;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Nickel-cobalt-cadmium resistance protein nccy.
GN NCCY.
OS Alcaligenes xylosoxydans xylosoxydans (Achromobacter xylosoxydans).
OG Plasmid pTOM9.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Achromobacter.
OX NCBI_TaxID=515;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=31A;
RX MEDLINE=95050278; PubMed=7961470;
RA Schmidt T., Schlegel H.G.;
RT "Combined nickel-cobalt-cadmium resistance encoded by the ncc locus
of Alcaligenes xylosoxydans 31A.";
RL J. Bacteriol. 176:7045-7054(1994).
CC -!- FUNCTION: COMPONENT OF THE NCC CATION-EFFLUX SYSTEM THAT CONFERS
RESISTANCE TO NICKEL, COBALT AND CADMIUM. MAY BE INVOLVED IN THE
REGULATION OF NCC.
CC -!- SIMILARITY: TO A.EUTROPHUS CNRY.
CC -----
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CC -----
DR EMBL; L31363; AAA65101.1; -.
DR PIR; I39575; I39575.
KW Plasmid; Nickel; Cobalt; Cadmium.
SQ SEQUENCE 95 AA; 10422 MW; 4524AA1F3EB37987 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 95;
Best Local Similarity 62.5%; Pred. No. 14;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KWLQLKK 9
Db 6 EWLVLQAKK 13

RESULT 12
RAC2_ARATH STANDARD; PRT; 201 AA.
AC Q38903;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RAC-like GTP binding protein ARAC2.
GN ARAC2 OR AT5G45970 OR MCL19.1.
OS Arabidopsis thaliana (Mouse-ear cress).
```

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=98009984; PubMed=9349271;
RA Winge P., Brembu T., Bones A.M.;
RT "Cloning and characterization of rac-like cDNAs from Arabidopsis
thaliana.";
RL Plant Mol. Biol. 35:483-495(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RA Winge P., Brembu T., Kristensen R., Bones A.M.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=98069011; PubMed=9405937;
RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.
Sequence features of the regions of 1,044,062 bp covered by thirteen
physically assigned pl clones.";
RL DNA Res. 4:291-300(1997).
CC -!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE ROOT, HYPOCOTYL
AND STEM.
CC -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
CC -----
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CC -----
DR EMBL; U43026; AAC49852.1; -.
DR EMBL; AF115469; AAF40241.1; -.
DR EMBL; AB006698; BAB08242.1; -.
DR PIR; T48862; T48862.
DR HSSP; P21181; 1AM4.
DR InterPro; IPR003578; GTPase_Rho.
DR InterPro; IPR001806; Ras_trnsmng.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00071; ras; 1.
DR PRINTS; PR00449; RASTRNSFRMNG.
DR SMART; SM00174; RHO; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
KW GTP-binding; Prenylation; Lipoprotein.
FT NP_BIND 13 20 GTP (BY SIMILARITY).
FT NP_BIND 60 64 GTP (BY SIMILARITY).
FT NP_BIND 118 121 GTP (BY SIMILARITY).
FT DOMAIN 35 43 EFFECTOR REGION (POTENTIAL).
FT LIPID 198 198 GERANYL-GERANYL (POTENTIAL).
SQ SEQUENCE 201 AA; 22393 MW; B3E73F55BDBB8028 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 201;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KWLQLKK 8
Db 98 KWLPELR 105

RESULT 13
V282_ARATH STANDARD; PRT; 209 AA.
ID V282_ARATH
AC O65421;
DT 16-OCT-2001 (Rel. 40, Created)
```

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE VPS28 protein homolog 2.
GN AT4C21560 OR F18E5.180 OR F17L22.20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Voickaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
RA Harris B., Ansong W., Brandt P., Grivoil L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robson J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weijens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooljman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlroy K., Mayes R.,
RA Pettiti A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Blocker H., Scharie M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,
RA Massenot O., Quigley F., Ciabaud G., Kuendlin A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chedfor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Hargues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle H., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Rielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegele L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisler C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matcra A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.;
RT *Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana.*;
RL Nature 402:769-777(1999).
CC -!- SIMILARITY: BELONGS TO THE VPS28 FAMILY.
CC -----
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CC -----
CC EMBL; AL022603; CAA18720.1; -
DR EMBL; AL035527; CAB36800.1; -
DR EMBL; AL161555; CAB81263.1; -
DR PIR; T05164; T05164.

DR Pfam; PF03997; VPS28; 1.
KW Hypothetical protein; Transport; Protein transport.
SQ SEQUENCE 209 AA; 23494 MW; 8A8BB4B415D9786B CRC64;

Query Match 68.8%; Score 33; DB 1; Length 209;
Best Local Similarity 55.6%; Pred. No. 29;
Matches 5; Conservative 3; Mismatches 1; Indels 0;
Gaps 0;

QY 1 KKWLQLKK 9
|:|:|:| |
Db 166 KEWLRLSK 174

RESULT 14
GCHI_PASMU STANDARD; PRT; 218 AA.
AC P57865;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE GTP cyclohydrolase I (EC 3.5.4.16) (GTP-CH-I).
GN FOLE OR PM0693.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT *Complete genomic sequence of Pasteurella multocida Pm70.*;
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -!- CATALYTIC ACTIVITY: GTP + 2 H(2)O -> formate + 2-amino-4-hydroxy-6-
CC (erythro-1,2,3-trihydroxypropyl) dihydropteridine triphosphate.
CC -!- PATHWAY: Tetrahydrofolate biosynthesis; first step.
CC -!- SUBUNIT: Homopolymer (By similarity).
CC -!- SIMILARITY: BELONGS TO THE GTP CYCLOHYDROLASE I FAMILY.
CC -----
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CC -----
CC EMBL; AE006106; AAK02777.1; -
DR HSSP; P27511; 1A8R.
DR HAMAP; MF_00223; -; 1.
DR InterPro; IPR001474; GTP_cyclohydrol1.
DR Pfam; PF01227; GTP_cyclohydrol1.
DR ProDom; PD003330; GTP_cyclohydrol1.
DR TIGRFAMs; TIGR00063; fole; 1.
DR PROSITE; PS00859; GTP_CYCLOHYDROL_1_1; 1.
DR PROSITE; PS00860; GTP_CYCLOHYDROL_1_2; 1.
KW One-carbon metabolism; Hydrolase; Complete proteome.
FT DISULFID 109 180 BY SIMILARITY.
SQ SEQUENCE 218 AA; 24953 MW; 12F1FC8129E790C9 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 2; Indels 0;
Gaps 0;

QY 1 KKWLQLKK 9
|:|:|:| |
Db 127 KKWVIGLSK 135

RESULT 15
EXOR_RHILV STANDARD; PRT; 267 AA.
ID EXOR_RHILV
AC Q52822;

DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Exopolysaccharide production negative regulator precursor.
GN EXOR.
OS Rhizobium leguminosarum (biovar viciae).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=387;
RN {1}
RP SEQUENCE FROM N.A.
RC STRAIN=WSM710 / WR6-35;
RX MEDLINE=97346048; PubMed=9202471;
RA Reeve W.G., Dilworth M.J., Tiwari R.P., Glenn A.R.;
RT "Regulation of exopolysaccharide production in Rhizobium leguminosarum
RT biovar viciae WSM710 involves exor.";
RL Microbiology 143:1951-1958(1997).
CC -!- FUNCTION: NEGATIVELY MODULATES EXOPOLYSACCHARIDE (EPS)
CC BIOSYNTHESIS.
CC -----
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CC -----
DR EMBL; L39937; AAB63941.1; -.
DR InterPro; IPR006597; Sel_like.
DR SMART; SM00671; SEL; 3.
KW Exopolysaccharide synthesis; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 267 EXOPOLYSACCHARIDE PRODUCTION NEGATIVE
FT REGULATOR.
SQ SEQUENCE 267 AA; 28922 MW; E45E2E0538E1F573 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 267;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKWLIIQLKK 9
| | | | | : |
Db 185 KKWLNQARK 193

Search completed: October 14, 2003, 14:34:06
Job time : 8.54167 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 ; Search time 29.8125 seconds
(without alignments)
77.903 Million cell updates/sec

Title: US-09-881-490-162
Perfect score: 48
Sequence: 1 KKWLIQLKK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SP TREMBL_23:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp Vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriaph:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|---------------------|
| 1 | 40 | 83.3 | 369 | 2 Q93CS6 | Q93cs6 shigella bo |
| 2 | 38 | 79.2 | 229 | 5 Q8MP31 | Q8mp31 dictyoste. |
| 3 | 37 | 77.1 | 189 | 16 Q821K3 | Q82lk3 salmonella |
| 4 | 37 | 77.1 | 275 | 16 Q9JYL8 | Q9jyl8 neisseria m |
| 5 | 36 | 75.0 | 89 | 2 Q9EYA7 | Q9eva7 escherichia |
| 6 | 36 | 75.0 | 278 | 4 Q9UJ05 | Q9ujc5 homo sapien |
| 7 | 36 | 75.0 | 284 | 4 Q96BV3 | Q96bv3 homo sapien |
| 8 | 36 | 75.0 | 459 | 10 Q8H3G5 | Q8h3g5 oryza sativ |
| 9 | 36 | 75.0 | 578 | 10 Q23488 | Q23488 arabidopsis |
| 10 | 36 | 75.0 | 652 | 5 Q8I427 | Q8i427 plasmodium |
| 11 | 36 | 75.0 | 1566 | 5 Q9N3E9 | Q9n3e9 caenorhabdi |
| 12 | 35 | 72.9 | 136 | 16 Q8E176 | Q8ei76 shewanella |
| 13 | 35 | 72.9 | 198 | 10 Q65062 | Q65062 picea maria |
| 14 | 35 | 72.9 | 261 | 16 Q9CNC3 | Q9cnc3 pasteurella |
| 15 | 35 | 72.9 | 294 | 8 Q8HIS8 | Q8his8 monosiqua br |
| 16 | 35 | 72.9 | 338 | 5 Q01679 | Q01679 bombyx mori |

| | | | | | |
|----|----|------|------|-----------|--------------------|
| 17 | 35 | 72.9 | 381 | 16 Q8DSD4 | Q8dsd4 streptococc |
| 18 | 35 | 72.9 | 585 | 16 Q66759 | Q66759 aquifex aeo |
| 19 | 35 | 72.9 | 643 | 5 Q8IIV6 | Q8iliv6 plasmodium |
| 20 | 35 | 72.9 | 731 | 10 Q9AW75 | Q9aw75 guillardia |
| 21 | 35 | 72.9 | 767 | 10 Q8GXD0 | Q8gxd0 arabidopsis |
| 22 | 35 | 72.9 | 2655 | 10 Q9C8A3 | Q9c8a3 arabidopsis |
| 23 | 34 | 70.8 | 59 | 16 Q8YW77 | Q8yw77 anabaena sp |
| 24 | 34 | 70.8 | 89 | 9 Q9XJ11 | Q9xjl1 bacterioph |
| 25 | 34 | 70.8 | 89 | 16 Q8XEh8 | Q8xeh8 escherichia |
| 26 | 34 | 70.8 | 115 | 16 Q8CV09 | Q8cv09 oceanobacil |
| 27 | 34 | 70.8 | 234 | 11 Q9D334 | Q9d334 mus musculu |
| 28 | 34 | 70.8 | 235 | 16 Q8XL88 | Q8xl88 clostridium |
| 29 | 34 | 70.8 | 245 | 4 Q60573 | Q60573 homo sapien |
| 30 | 34 | 70.8 | 245 | 11 Q88503 | Q88503 mus musculu |
| 31 | 34 | 70.8 | 245 | 11 Q8BMB3 | Q8bmb3 mus musculu |
| 32 | 34 | 70.8 | 276 | 16 Q9JTL7 | Q9jtl7 neisseria m |
| 33 | 34 | 70.8 | 285 | 16 Q31436 | Q31436 bacillus su |
| 34 | 34 | 70.8 | 287 | 16 Q98QY4 | Q98qy4 mycoplasma |
| 35 | 34 | 70.8 | 343 | 1 Q9HH38 | Q9hh38 methanobact |
| 36 | 34 | 70.8 | 432 | 2 Q8GCX1 | Q8gcx1 enterococcu |
| 37 | 34 | 70.8 | 521 | 5 Q9VPX7 | Q9vpx7 drosophila |
| 38 | 34 | 70.8 | 526 | 4 Q9Y3N2 | Q9y3n2 homo sapien |
| 39 | 34 | 70.8 | 547 | 16 Q8XE44 | Q8xe44 escherichia |
| 40 | 34 | 70.8 | 547 | 16 Q8FEQ4 | Q8ffq4 escherichia |
| 41 | 34 | 70.8 | 732 | 16 Q99XP7 | Q99xp7 streptococc |
| 42 | 34 | 70.6 | 732 | 16 Q8K5K3 | Q8k5k3 streptococc |
| 43 | 34 | 70.8 | 839 | 5 Q961M8 | Q961m8 drosophila |
| 44 | 34 | 70.8 | 954 | 4 Q8WXXV8 | Q8wxv8 homo sapien |
| 45 | 34 | 70.8 | 957 | 4 Q9H0V3 | Q9h0v3 homo sapien |

ALIGNMENTS

RESULT 1
Q93CS6 PRELIMINARY; PRT: 369 AA.
ID Q93CS6
AC Q93CS6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative glycosyl transferase.
GN WBAT.
OS Shigella boydii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21481970; PubMed=11598067;
RA Wang L., Qu W., Reeves P.R.;
RT "Sequence Analysis of Four Shigella boydii O-Antigen Loci: Implication for Escherichia coli and Shigella Relationships.";
RL Infect. Immun. 69:6923-6930(2001).
DR EMBL; AF402314; AAL27338.1; -
DR InterPro; IPR001296; Glyco_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Transferase.
SQ SEQUENCE 369 AA; 42760 MW; 3E2CCE371A6BA0BB CRC64;

Query Match 83.3%; Score 40; DB 2; Length 369;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLIQLKK 9
|||||:
Db 359 KKWLIKLRQ 367

RESULT 2
Q8MP31 PRELIMINARY; PRT: 229 AA.
ID Q8MP31
AC Q8MP31;

DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and Analysis of Chromosome 2 of Dictyostelium";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC117178; AAM44388.1; -;
DR InterPro: IPR001064; Crystallin.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 1.
KW Hypothetical protein.
SQ SEQUENCE 229 AA; 27735 MW; FDCLE5C8B9647DD6 CRC64;

Query Match 79.2%; Score 38; DB 5; Length 229;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLIQLKK 9
Db 119 KRWLTEIKK 127
|||||

RESULT 3

Q821K3 ID Q821K3 PRELIMINARY; PRT; 189 AA.
AC Q821K3;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE Putative membrane protein.
GN STY4561.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL: AL627282; CAP09337.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 189 AA; 22077 MW; C817745ABC69BE2A CRC64;

Query Match 77.1%; Score 37; DB 16; Length 189;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLIQLKK 9
Db 101 KRWLIQAKR 109
|||||

RESULT 4

Q9JYL8

ID Q9JYL8 PRELIMINARY; PRT; 275 AA.
AC Q9JYL8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Phycoene synthase-related protein.
GN NMB1521.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gunn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Citterone H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Pizza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58.";
RL Science 287:1809-1815(2000).
DR EMBL: AE002501; AAF41877.1; -;
DR TIGR: NMB1521; -;
DR InterPro: IPR002060; Squ/phyt_synthse.
DR Pfam: PF00494; SQS_PSY; 1.
KW Complete proteome.
SQ SEQUENCE 275 AA; 30613 MW; B8B2C2D77A549EA6 CRC64;

Query Match 77.1%; Score 37; DB 16; Length 275;
Best Local Similarity 77.8%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKWLIQLKK 9
Db 263 KDWLIMLKK 271
|||||

RESULT 5

Q9EYA7 ID Q9EYA7 PRELIMINARY; PRT; 89 AA.
AC Q9EYA7;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Kil protein.
GN KIL.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7;
RX MEDLINE=20564182; PubMed=11111050;
RA Yokoyama K., Makino K., Kubota Y., Watanabe M., Kimura S.,
RA Yutsudo C.H., Kurokawa K., Ishii K., Hattori M., Abe H., Iida T.,
RA Yamamoto K., Hayashi T., Yasunaga T., Honda T., Sasakawa C.,
RA Shinagawa H.;
RT "Complete nucleotide sequence of the defective Sakai-VT1 prophage
carrying the shiga toxin 1 genes of the enterohemorrhagic Escherichia
coli O157:H7 derived from the Sakai outbreak.";
RL Gene 258:127-139(2000).
DR EMBL: AP000400; BAB19614.1; -;
SQ SEQUENCE 89 AA; 10127 MW; CD30904BF080D5FD CRC64;

Query Match 75.0%; Score 36; DB 2; Length 89;
Best Local Similarity 55.6%; Pred. No. 33;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KWLQLKK 9
| | | | |
Db 74 KWLMLKR 82

RESULT 6
Q9UJ05 PRELIMINARY; PRT; 278 AA.
AC Q9UJ05;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE DJ486I3.1 (Novel protein) (Fragment).
GN DJ486I3.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (AUG-1999) to the EMBL/GenBank/CDRJ databases.
DR EMBL; AL050331; CAB55880.1; -.
FT NON_TER 1
SQ SEQUENCE 278 AA; 31677 MW; 0088AFF6B3BC3F6F CRC64;

Query Match 75.0%; Score 36; DB 4; Length 278;
Best Local Similarity 87.5%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KWLQLKK 8
| | | | |
Db 25 KWLRLKK 32

RESULT 7
Q96BV3 PRELIMINARY; PRT; 284 AA.
AC Q96BV3;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bladder;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015138; AAH15138.1; -.
KW Hypothetical protein.
SQ SEQUENCE 284 AA; 32370 MW; BCD8F0A67699530A CRC64;

Query Match 75.0%; Score 36; DB 4; Length 284;
Best Local Similarity 87.5%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KWLQLKK 8
| | | | |
Db 31 KWLRLKK 38

RESULT 8
Q8H3G5 PRELIMINARY; PRT; 459 AA.
AC Q8H3G5;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)

DE OSJNB0062D12.24 protein.
GN OSJNB0062D12.24.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
clone:OSJNB0062D12.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005127; BAC16708.1; -.
SQ SEQUENCE 459 AA; 51464 MW; 5D66AF12D91CF90F CRC64;

Query Match 75.0%; Score 36; DB 10; Length 459;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KWLQLKK 9
| | | | |
Db 322 KWLRLKK 329

RESULT 9
O23488 PRELIMINARY; PRT; 578 AA.
AC O23488;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein (LET1 like protein).
GN AT4G16440.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98121113; PubMed=9461215;
RA Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,
RA Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,
RA Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,
RA Wedler E., Wambutt R., Weitzenecker T., Pohl T.M., Terry N.,
RA Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
RA Auborg S., Gy I., Kreis M., Kavanagh T., Hempel S., Kotter P.,
RA Entian K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,
RA Silvey M., James R., Montfort A., Pons A., Pulgdomenech P., Douka A.,
RA Voukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermaier B.,
RA Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,
RA Palme K., Benes V., Rechman S., Ansoerge W., Cooke R., Berger C.,
RA Delseny M., Voet M., Volckaert G., Mewes H.W., Klosterman S.,
RA Schueller C., Chalwatzis N.;
RT "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
Arabidopsis thaliana.";
RL Nature 391:485-488(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z97341; CAB10420.1; -.
DR EMBL; AL161544; CAB78686.1; -.
DR InterPro; IPR006459; DUF_A_thal_1569.
DR InterPro; IPR003149; Fe_hyd_SSU.
DR Pfam; PF02256; Fe_hyd_SSU; 1.
DR TIGRFAMs; TIGR01569; A_tha_TIGR01569; 1.
SQ SEQUENCE 578 AA; 64340 MW; 212385A45DC3C09A CRC64;

Query Match 75.0%; Score 36; DB 10; Length 578;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;

| Matches | | 7; | Conservative | 0; | Mismatches | 1; | Indels | 0; | Gaps | 0; |
|--|---|------------------|--------------|----|------------|----|--------|----|------|----|
| QY | Db | 2 KWLQQLKK 9 | | | | | | | | |
| | | 30 KWLQQLKK 37 | | | | | | | | |
| | | | | | | | | | | |
| RESULT 10 | | | | | | | | | | |
| Q8I427 PRELIMINARY; PRT; 652 AA. | | | | | | | | | | |
| ID | Q8I427 | | | | | | | | | |
| AC | Q8I427; | | | | | | | | | |
| DT | 01-MAR-2003 (TREMBlrel. 23, Created) | | | | | | | | | |
| DT | 01-MAR-2003 (TREMBlrel. 23, Last sequence update) | | | | | | | | | |
| DT | 01-MAR-2003 (TREMBlrel. 23, Last annotation update) | | | | | | | | | |
| DE | Cell differentiation protein rcd1, putative. | | | | | | | | | |
| GN | PF0375W. | | | | | | | | | |
| OS | Plasmodium falciparum (isolate 3D7). | | | | | | | | | |
| OC | Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. | | | | | | | | | |
| OX | NCBI_TaxID=36329; | | | | | | | | | |
| RN | {1} | | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | | |
| RA | Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A., | | | | | | | | | |
| RA | Hall N., Bowman S., Churcher C., Quail M., Barrell B., | | | | | | | | | |
| RL | Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases. | | | | | | | | | |
| RN | {2} | | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | | |
| RX | MEDLINE-22255708; PubMed-12368867; | | | | | | | | | |
| RA | Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D., | | | | | | | | | |
| RA | Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K., | | | | | | | | | |
| RA | Buckee C.O., Burrows C., Cherevach I., Chillingworth C., | | | | | | | | | |
| RA | Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C., | | | | | | | | | |
| RA | Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J., | | | | | | | | | |
| RA | Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z., | | | | | | | | | |
| RA | Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P., | | | | | | | | | |
| RA | Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A., | | | | | | | | | |
| RA | Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N., | | | | | | | | | |
| RA | Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L., | | | | | | | | | |
| RA | Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E., | | | | | | | | | |
| RA | Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M., | | | | | | | | | |
| RA | Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K., | | | | | | | | | |
| RA | Taylor K., Tivey A., Unwin I., Whitehead S., Woodward J., | | | | | | | | | |
| RA | Sulston J.E., Craig A., Newbold C., Barrell B.G; | | | | | | | | | |
| RT | *Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.*; | | | | | | | | | |
| RL | Nature 419:527-531(2002). | | | | | | | | | |
| DR | EMBL; AL929351; CAD51441.1; - | | | | | | | | | |
| SQ | SEQUENCE 652 AA; 73423 MW; 90BBF62FBFB7FF7F CRC64; | | | | | | | | | |
| Query Match 75.0%; Score 36; DB 5; Length 652; | | | | | | | | | | |
| Best Local Similarity 85.7%; Pred. NO. 2.1e+02; | | | | | | | | | | |
| Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | | |
| QY | 1 KWLQQL 7 | | | | | | | | | |
| Db | 482 KWLQQL 488 | | | | | | | | | |
| | | | | | | | | | | |
| RESULT 11 | | | | | | | | | | |
| Q9N3E9 PRELIMINARY; PRT; 1566 AA. | | | | | | | | | | |
| ID | Q9N3E9 | | | | | | | | | |
| AC | Q9N3E9; | | | | | | | | | |
| DT | 01-OCT-2000 (TREMBlrel. 15, Created) | | | | | | | | | |
| DT | 01-OCT-2001 (TREMBlrel. 18, Last sequence update) | | | | | | | | | |
| DT | 01-MAR-2003 (TREMBlrel. 23, Last annotation update) | | | | | | | | | |
| DE | Hypothetical 180.6 kDa protein. | | | | | | | | | |
| GN | Y54E10A.11. | | | | | | | | | |
| OS | Caenorhabditis elegans. | | | | | | | | | |
| OC | Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; | | | | | | | | | |
| OC | Rhabditidae; Peloderinae; Caenorhabditis. | | | | | | | | | |
| OX | NCBI_TaxID=6239; | | | | | | | | | |
| RN | {1} | | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | | |
| RC | STRAIN-Bristol N2; | | | | | | | | | |
| RX | MEDLINE-99069613; PubMed-9851916; | | | | | | | | | |

| | |
|--|---|
| RA | None; |
| RI | "Genome sequence of the nematode C. elegans: a platform for |
| RI | investigating biology. The C. elegans Sequencing Consortium.*; |
| RL | Science 282:2012-2018(1998). |
| RN | {2} |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN-Bristol N2; |
| RA | Wollam A., Becker M., Graves T., Hawkins M.; |
| RI | "The sequence of C. elegans cosmid Y54E10A.*; |
| RL | Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases. |
| RN | {3} |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN-Bristol N2; |
| RA | Waterston R.; |
| RT | "Direct Submission.*; |
| RL | Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases. |
| DR | EMBL; AC024810; AAF60772.2; - |
| DR | WormPep; Y54E10A.11; CE29120. |
| DR | InterPro; IPR001841; 2nf_ring. |
| DR | SMART; SM00184; RING; 1. |
| DR | PROSITE; PS50089; ZF_RING_2; 1. |
| KW | Hypothetical protein. |
| SQ | SEQUENCE 1566 AA; 180607 MW; F7D21D6EC9BA0F16 CRC64; |
| Query Match 75.0%; Score 36; DB 5; Length 1566; | |
| Best Local Similarity 85.7%; Pred. No. 4.7e+02; | |
| Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; | |
| QY | 1 KKWLIQL 7 |
| | |
| Db | 1477 KKWLIQL 1483 |
| RESULT 12 | |
| Q8EI76 | ID Q8EI76 PRELIMINARY; PRT: 136 AA. |
| AC | Q8EI76; |
| DT | 01-MAR-2003 (TREMBlrel. 23, Created) |
| DT | 01-MAR-2003 (TREMBlrel. 23, Last sequence update) |
| DT | 01-MAR-2003 (TREMBlrel. 23, Last annotation update) |
| DE | Hypothetical protein. |
| GN | SO0971. |
| OS | Shewanella oneidensis. |
| OC | Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; |
| OC | Alteromonadaceae; Shewanella. |
| OX | NCBI_TaxID=70863; |
| RN | {1} |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN-MR-1; |
| RX | MEDLINE-22297686; PubMed-12368813; |
| RA | Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., |
| RA | Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., |
| RA | Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., |
| RA | DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., |
| RA | Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., |
| RA | Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., |
| RA | Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., |
| RA | Feldblyum T.V., Smith H.O., Venter J.C., Nelson K.H., Fraser C.M.; |
| RT | "Genome sequence of the dissimilatory metal ion-reducing bacterium |
| RT | Shewanella oneidensis.*; |
| RL | Nat. Biotechnol. 20:1118-1123(2002). |
| DR | EMBL; AE015542; AAN54045.1; - |
| DR | TIGR; SO0971; - |
| KW | Hypothetical protein; Complete proteome. |
| SQ | SEQUENCE 136 AA; 15529 MW; 420710910979605C CRC64; |
| Query Match 72.9%; Score 35; DB 16; Length 136; | |
| Best Local Similarity 85.7%; Pred. No. 75; | |
| Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; | |

RESULT 13

O65062 ID O65062 PRELIMINARY; PRT; 198 AA.
AC O65062;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rac-like GIP binding protein.
GN SB30.
OS Picea mariana (Black spruce).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98278823; PubMed=9611216;
RA Perry D.J., Bousquet J.;
RT "Sequence-tagged-site (STS) markers of arbitrary genes. Development,
RT characterization and analysis of linkage in black spruce.";
RL Genetics 149:1089-1098(1998).
CC -1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
DR EMBL; AF051223; AAC32124.1; -;
DR HSSP; P21181; IAM4.
DR InterPro; IPR003578; GTPase_Rho.
DR InterPro; IPR001806; Ras_trnsmg.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00071; ras; 1.
DR PRINTS; PR00449; RASTRNSFRMG.
DR SMART; SM00174; RHO; 1.
DR TIGRFAMs; TIGR00231; small_gtp; 1.
KW GTP-binding; Lipoprotein; Prenylation.
SQ SEQUENCE 198 AA; 21997 MW; FA72F6EBB1D15E45 CRC64;

Query Match 72.9%; Score 35; DB 10; Length 198;
Best Local Similarity 62.5%; Pred. No. 1.1e-02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLK 8

Db 98 KKWLLELR 105

RESULT 14

Q9CNC3 ID Q9CNC3 PRELIMINARY; PRT; 261 AA.
AC Q9CNC3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein PM0509.
GN PM0509.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE005086; AAK02593.1; -;
DR InterPro; IPR002654; Glyco_trans_25.
DR Pfam; PF01755; Glyco_transf_25; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 261 AA; 30190 MW; 6D71C37C615FEF44 CRC64;

Query Match 72.9%; Score 35; DB 16; Length 261;
Best Local Similarity 66.7%; Pred. No. 1.4e-02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9

Db 2 QKWLSLEK 10

RESULT 15

Q8HIS8 ID Q8HIS8 PRELIMINARY; PRT; 294 AA.
AC Q8HIS8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Orf294.
GN ORF294.
OS Monosiga brevicollis.
OG Mitochondrion.
OC Eukaryota; Choanoflagellida; Codonosigidae; Monosiga.
OX NCBI_TaxID=81824;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20377911; PubMed=10916154;
RA Bullerwell C.E., Burger G., Lang B.F.;
RT "A novel motif for identifying rps3 homologs in fungal mitochondrial
RT genomes.";
RL Trends Biochem. Sci. 25:363-365(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Lang B.F., O'Kelly C.J., Nerad T.A., Gray M.W., Burger G.;
RL "The closest unicellular relatives of animals.";
RL Curr. Biol. 0:0-0(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Lang F.B., Bullerwell C.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DDIJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Burger G., Lang B.F.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DDIJ databases.
DR EMBL; AF538053; AAN28356.1; -;
KW Mitochondrion.
SQ SEQUENCE 294 AA; 34521 MW; 6CD1601F13C6D9D6 CRC64;

Query Match 72.9%; Score 35; DB 8; Length 294;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLK 8

Db 30 KKWIITLK 37

Search completed: October 14, 2003, 14:36:55
Job time : 32.8125 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:19 ; Search time 38.625 Seconds
(without alignments)
36.985 Million cell updates/sec

Title: US-09-881-490-163
Perfect score: 48
Sequence: 1 KKLQILWKK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*

10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*

12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

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21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|---------------------|
| 1 | 48 | 100.0 | 9 | 17 AAW04048 | Antifungal peptide |
| 2 | 48 | 100.0 | 9 | 18 AAW44562 | Anti-fungal peptid |
| 3 | 48 | 100.0 | 9 | 20 AAY00539 | Antifungal peptide |
| 4 | 48 | 100.0 | 9 | 22 AAB65463 | Anti-fungal peptid |
| 5 | 43 | 89.6 | 8 | 18 AAW44604 | Anti-fungal peptide |
| 6 | 43 | 89.6 | 8 | 20 AAY00581 | Antifungal peptide |
| 7 | 43 | 89.6 | 8 | 22 AAB65505 | Anti-fungal peptid |
| 8 | 43 | 89.6 | 9 | 18 AAW44606 | Anti-fungal peptide |
| 9 | 43 | 89.6 | 9 | 20 AAY00583 | Antifungal peptide |

| | | | | | | |
|----|----|------|------|----|----------|--------------------|
| 10 | 43 | 89.6 | 9 | 22 | AAB65507 | Anti-fungal peptid |
| 11 | 38 | 79.2 | 128 | 22 | AAO00543 | Human polypeptide |
| 12 | 38 | 79.2 | 325 | 23 | ABG65564 | Human breast speci |
| 13 | 38 | 79.2 | 369 | 22 | ABG15487 | Novel human diagno |
| 14 | 38 | 79.2 | 414 | 22 | ABG15486 | Novel human diagno |
| 15 | 36 | 75.0 | 547 | 23 | ABB05745 | Mouse zcytor17 pro |
| 16 | 36 | 75.0 | 662 | 23 | ABB05742 | Mouse zcytor17 pro |
| 17 | 36 | 75.0 | 716 | 24 | ABP54370 | Mouse mNR10Balb-c |
| 18 | 36 | 75.0 | 716 | 24 | ABP54371 | Mouse mNR10c57BL-6 |
| 19 | 36 | 75.0 | 726 | 23 | AAE24037 | Mouse haematopoiet |
| 20 | 36 | 75.0 | 2086 | 22 | ABB64128 | Drosophila melanog |
| 21 | 35 | 72.9 | 55 | 21 | AAG01005 | Human secreted pro |
| 22 | 35 | 72.9 | 145 | 22 | AAO01497 | Human polypeptide |
| 23 | 35 | 72.9 | 303 | 20 | AAW88847 | Polypeptide fragme |
| 24 | 35 | 72.9 | 303 | 22 | ABB50865 | Human secreted pro |
| 25 | 35 | 72.9 | 400 | 20 | AAW88851 | Polypeptide fragme |
| 26 | 35 | 72.9 | 400 | 22 | ABB50869 | Human secreted pro |
| 27 | 35 | 72.9 | 492 | 22 | ABG03810 | Novel human diagno |
| 28 | 35 | 72.9 | 492 | 22 | ABG14087 | Novel human diagno |
| 29 | 35 | 72.9 | 738 | 20 | AAW95332 | Human phospholipas |
| 30 | 35 | 72.9 | 740 | 21 | AAW58878 | Human peptidase NA |
| 31 | 35 | 72.9 | 740 | 22 | AAW24008 | Human EST encoded |
| 32 | 35 | 72.9 | 740 | 22 | AAB88354 | Human membrane or |
| 33 | 35 | 72.9 | 795 | 21 | AAW95968 | Human TANGO 243. |
| 34 | 35 | 72.9 | 795 | 22 | AAB93162 | Human protein sequ |
| 35 | 35 | 72.9 | 795 | 22 | AAB68514 | Human GTP-binding |
| 36 | 35 | 72.9 | 855 | 21 | AAW95969 | Human TANGO 243 (a |
| 37 | 34 | 70.8 | 18 | 21 | AAB22991 | Amphipathic cation |
| 38 | 34 | 70.8 | 20 | 19 | AAW65895 | Amphipathic peptid |
| 39 | 34 | 70.8 | 20 | 21 | AAW49957 | Amphipathic peptid |
| 40 | 34 | 70.8 | 45 | 21 | AAG07026 | Arabidopsis thalia |
| 41 | 34 | 70.8 | 49 | 22 | ABG58565 | Human liver peptid |
| 42 | 34 | 70.8 | 49 | 22 | ABB43169 | Peptide #10675 enc |
| 43 | 34 | 70.8 | 49 | 22 | ABB26273 | Protein #8272 enco |
| 44 | 34 | 70.8 | 49 | 22 | AAW64078 | Human brain expres |
| 45 | 34 | 70.8 | 49 | 22 | AAW76899 | Human bone marrow |

ALIGNMENTS

RESULT 1
AAW04048
ID AAW04048 standard; peptide; 9 AA.

XX AAW04048;

AC AAW04048;

XX 04-NOV-1996 (first entry)

XX Antifungal peptide XMP.332.

DE Antifungal peptide; inhibitor; Domain III; polymorphonuclear leukocyte;
KW bactericidal/permeability-increasing protein; BPI; mammalian; PMN; fungi;
KW neutrophil; replication inhibitor; fungal infection; Aspergillus;
KW Cryptococcus; Candida; C.albicans; C.galabrat; C.krusei; C.lusitaniae;
KW C.parapsilosis; C.tropicalis; therapy.

OS Synthetic.

XX

FH Key Location/Qualifiers
FT Misc-difference 1..9 /note= "D-form residues"
FT Modified-site 9 /note= "amidated"

XX WO9608509-A1.

XX 21-MAR-1996.

XX 20-JUL-1995; 95WO-US09262.

XX 13-JAN-1995; 95US-0372105.

PR 15-SEP-1994; 94US-0306473.

XX (XOMA) XOMA CORP.
XX PA
XX PI Fadem MB, Lim E, Little RG;
XX XX
XX WPI; 1996-179900/18.
XX Antifungal peptide(s) derived from Domain III of BPI protein - used
PT in vitro for killing or inhibiting replication of fungi, esp.
PT Candida species
XX XX
XX Claim 9; Page 155; 199pp; English.
XX XX
XX AAW04000-W04160 represent antifungal peptides. These sequences are
CC based on (or derived from) Domain III of the
CC bactericidal/permeability-increasing protein (BPI). BPI is a protein
CC that can be isolated from the granules of mammalian polymorphonuclear
CC leukocytes (PMNs or neutrophils). These antifungal peptides can be used
CC for killing, or inhibiting replication of, fungi in vitro. These
CC sequences can also be used for treatment of a fungal infection involving
CC fungi from the species Candida, Aspergillus and Cryptococcus. The
CC sequences are especially useful for treating C.albicans, C.galabrat,
CC C.krusei, C.lusitaniae, C.parapsilosis and C.tropicalis infections.
XX XX
XX SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLQILWKK 9
Db 1 KKLQILWKK 9
RESULT 2
AAW44562
ID AAW44562 standard; peptide; 9 AA.
XX XX
AC AAW44562:
XX XX
DT 27-APR-1998 (first entry)
XX XX
DE Anti-fungal peptide #163 based on BPI protein (residues 142-169).
XX XX
KW Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.
XX XX
OS Synthetic.
OS Mammalia.
XX XX
XX Key Location/Qualifiers
FT Misc-difference 1..9 /note= "D-form residues"
FT Modified-site 9 /note= "C-terminal amide"
FT FT
XX XX
XX WO9704008-A1.
XX XX
XX 06-FEB-1997.
XX XX
XX 21-MAR-1996; 96WO-US03845.
XX XX
XX 20-JUL-1995; 95US-0504841.
XX XX
XX (XOMA) XOMA CORP.
XX XX
XX Fadem MB, Lim E, Little RG;
XX WPI; 1997-132578/12.
XX Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or

PT in vivo as a fungicides
XX XX
XX PS Claim 1; Page 192; 230pp; English.
XX XX
XX This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.
XX XX
XX SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLQILWKK 9
Db 1 KKLQILWKK 9
RESULT 3
AAW00539
ID AAW00539 standard; Peptide; 9 AA.
XX XX
AC AAW00539;
XX XX
DT 07-MAY-1999 (first entry)
XX XX
DE Antifungal peptide XMP.332.
XX XX
KW Antifungal; BPI; bactericidal/permeability increasing protein;
KW Candida infection.
XX XX
OS Synthetic.
XX XX
PN US5858974-A.
XX XX
PD 12-JAN-1999.
XX XX
PF 21-MAR-1996; 96US-0621259.
XX XX
PR 21-MAR-1996; 96US-0621259.
PR 20-JUL-1995; 95US-0504841.
XX XX
XX (XOMA) XOMA CORP.
XX XX
XX Fadem MB, Lim E, Little RG;
XX XX
XX WPI: 1999-119956/10.
XX XX
XX Antifungal peptides - comprising part of bactericidal or
PT permeability-increasing protein sequence or related sequence
XX XX
XX PS Disclosure; Columns 167-168; 132pp; English.
XX XX
XX New peptides are provided which are based on Domain III (amino acids
CC 142-169) of human bactericidal/permeability-increasing protein (BPI).
CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGLIQLFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, IQLF, WLIQL, LIQLF and WLIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of
CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitaniae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,

CC optionally together with a non-peptide antifungal agent.

XX Sequence 9 AA;

Query Match 100.0%; Score 48; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
| | | | | | | |
Db 1 KKLQILWKK 9

RESULT 4
AAB65463
ID AAB65463 standard; Peptide: 9 AA.

XX AAB65463;

DT 27-MAR-2001 (first entry)

DE Anti-fungal peptide XMP.332.

XX Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;
KW bactericidal/permeability-increasing protein; bactericidal;
KW fungal infection.

XX Homo sapiens.

OS US6156730-A.

PN 05-DEC-2000.

PD 08-JAN-1999; 99US-0227659.

XX 21-MAR-1996; 96US-0621259.

PR 12-MAR-1993; 93US-0030644.

PR 15-JUL-1993; 93US-0093202.

PR 14-JAN-1994; 94US-0183222.

PR 11-MAR-1994; 94US-0209762.

PR 11-JUL-1994; 94US-0273540.

PR 15-SEP-1994; 94US-0306473.

PR 13-JAN-1995; 95US-0372105.

PR 20-JUL-1995; 95US-0504841.

XX (XOMA) XOMA CORP.

PA Lim E, Fadem MB, Little RG;

PI WPI; 2001-090160/10.

XX Novel anti-fungal peptides derived from domain III of
PT bactericidal/permeability-increasing protein useful for killing or
PT inhibiting replication of fungi and for treating fungal infections -
XX Example 2; Columns 171-172; 134pp; English.
PS The present invention relates to antifungal peptides (see
XX AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C.albicans, C.glabrata, C.krusei,
CC C.lusitanae, C.parapsilosis and C.tropicalis.

XX Sequence 9 AA;

Query Match 100.0%; Score 48; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
| | | | | | | |
Db 1 KKLQILWKK 9

RESULT 5
AAW44604
ID AAW44604 standard; peptide; 8 AA.
XX AC AAW44604;

XX 27-APR-1998 (first entry)

DE Anti-fungal peptide #205 based on BPI protein (residues 142-169).

XX Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.

XX Synthetic.

OS Mammalia.

XX Key Location/Qualifiers

FT Misc-difference 1..8

FT Modified-site 8 /note= "D-form residues"

FT /note= "C-terminal amide"

XX WO9704008-A1.

XX 06-FEB-1997.

XX 21-MAR-1996; 96WO-US03845.

XX 20-JUL-1995; 95US-0504841.

XX (XOMA) XOMA CORP.

XX Fadem MB, Lim E, Little RG;

XX WPI; 1997-132578/12.

XX Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides

XX Claim 1; -pp; 230pp; English.

XX This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.

XX Sequence 8 AA;

Query Match 89.6%; Score 43; DB 18; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKLQILWKK 9
| | | | | | | |
Db 1 KKLQILWKK 8

RESULT 6
AAY00581
ID AAY00581 standard; Peptide; 8 AA.
XX AC AAY00581;

XX 07-MAY-1999 (first entry)
XX Antifungal peptide XMP.374.
DE Antifungal peptide XMP.374.
XX Antifungal; BPI; bactericidal/permeability increasing protein;
KW Candida infection.
XX Synthetic.
OS US5858974-A.
PN 12-JAN-1999.
XX 21-MAR-1996; 96US-0621259.
PD 21-MAR-1996; 96US-0621259.
PF 20-JUL-1995; 95US-0504841.
XX (XOMA) XOMA CORP.
PA Fadem MB, Lim E, Little RG;
XX WPI; 1999-119956/10.
DR Antifungal peptides - comprising part of bactericidal or
XX permeability-increasing protein sequence or related sequence
PT Claim 2; Columns 197-198; 132pp; English.
PS New peptides are provided which are based on Domain III (amino acids
XX 142-169) of human bactericidal/permeability-increasing protein (BPI).
CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGWLIQLFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, IQLF, WLIQL, LIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of
CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.
XX
SQ Sequence 8 AA;
Query Match 89.6%; Score 43; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KIQILWKK 9
Db 1 KIQILWKK 8
RESULT 7
AAB65505
ID AAB65505 standard; peptide: 8 AA.
XX AAB65505;
AC 27-MAR-2001 (first entry)
XX Anti-fungal peptide XMP.374.
DE Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;
KW bactericidal/permeability-increasing protein; bactericidal;
KW fungal infection.
XX Homo sapiens.
OS

XX US6156730-A.
PN 05-DEC-2000.
XX 08-JAN-1999; 99US-0227659.
PD 21-MAR-1996; 96US-0621259.
XX 12-MAR-1993; 93US-0030644.
PR 15-JUL-1993; 93US-0093202.
PR 14-JAN-1994; 94US-0183222.
PR 11-MAR-1994; 94US-0209762.
PR 11-JUL-1994; 94US-0273540.
PR 15-SEP-1994; 94US-0306473.
PR 13-JAN-1995; 95US-0372105.
PR 20-JUL-1995; 95US-0504841.
XX (XOMA) XOMA CORP.
PA Lim E, Fadem MB, Little RG;
XX WPI; 2001-090160/10.
DR Novel anti-fungal peptides derived from domain III of
XX bactericidal/permeability-increasing protein useful for killing or
XX inhibiting replication of fungi and for treating fungal infections -
PS Example 2; Columns 203-204; 134pp; English.
XX The present invention relates to antifungal peptides (see
CC AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C. albicans, C. glabrata, C. krusei,
CC C. lusitanae, C. parapsilosis and C. tropicalis.
XX
SQ Sequence 8 AA;
Query Match 89.6%; Score 43; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KIQILWKK 9
Db 1 KIQILWKK 8
RESULT 8
AAW44606
ID AAW44606 standard; peptide: 9 AA.
XX AAW44606;
AC 27-APR-1998 (first entry)
XX Anti-fungal peptide #207 based on BPI protein (residues 142-169).
DE Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
XX polymorphonuclear leukocyte; fungicide.
KW Synthetic.
XX Mammalia.
OS
OS
XX Key Location/Qualifiers
FT Misc-difference 1.9 /note= "D-form residues"
FT Modified-site 9 /note= "C-terminal amide"
FT

XX WO9704008-A1.
PN 06-FEB-1997.
XX 21-MAR-1996; 96WO-US03845.
PF 20-JUL-1995; 95US-0504841.
PR (XOMA) XOMA CORP.
XX Fadem MB, Lim E, Little RG;
PI WPI; 1997-132578/12.
DR Anti-fungal peptide(s) derived from or based on domain III of
XX bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides
PT
XX
PS Claim 1; -PP; 230pp; English.
XX This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.
XX
SQ Sequence 9 AA;
Query Match 89.6%; Score 43; DH 18; Length 9;
Best Local Similarity 88.9%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KKLQILWKK 9
Db 1 KKLQIAWKK 9
RESULT 9
AAY00583
ID AAY00583 standard; Peptide: 9 AA.
XX
AC AAY00583;
XX 07-MAY-1999 (first entry)
XX Antifungal peptide XMP.376.
DE Antifungal; BPI; bactericidal/permeability increasing protein;
XX Candida infection.
KW Synthetic.
XX US5858974-A.
PN 12-JAN-1999.
PD 21-MAR-1996; 96US-0621259.
XX 21-MAR-1996; 96US-0621259.
PF 20-JUL-1995; 95US-0504841.
XX (XOMA) XOMA CORP.
PA Fadem MB, Lim E, Little RG;
XX WPI; 1999-119956/10.
DR Antifungal peptides - comprising part of bactericidal or
XX permeability-increasing protein sequence or related sequence
PT
XX

PS Claim 2; Columns 199-200; 132pp; English.
XX New peptides are provided which are based on Domain III (amino acids
CC 142-169) of human bactericidal/permeability-increasing protein (BPI).
CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGWLIQIFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, IQLF, WLIQL, LIQLF and WLIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of
CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.
XX
SQ Sequence 9 AA;
Query Match 89.6%; Score 43; DB 20; Length 9;
Best Local Similarity 88.9%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KKLQILWKK 9
Db 1 KKLQIAWKK 9
RESULT 10
AAB65507
ID AAB65507 standard; Peptide: 9 AA.
XX
AC AAB65507;
XX 27-MAR-2001 (first entry)
XX Anti-fungal peptide XMP.376.
DE Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;
KW bactericidal/permeability-increasing protein; bactericidal;
KW fungal infection.
XX Homo sapiens.
OS US6156730-A.
PN 05-DEC-2000.
PD 08-JAN-1999; 99US-0227659.
PF 21-MAR-1996; 96US-0621259.
XX 12-MAR-1993; 93US-0030644.
PR 15-JUL-1993; 93US-0093202.
PR 14-JAN-1994; 94US-0183222.
PR 11-MAR-1994; 94US-0209762.
PR 11-JUL-1994; 94US-0273540.
PR 15-SEP-1994; 94US-0306473.
PR 13-JAN-1995; 95US-0372105.
PR 20-JUL-1995; 95US-0504841.
XX (XOMA) XOMA CORP.
PA Lim E, Fadem MB, Little RG;
XX WPI; 2001-090160/10.
DR Novel anti-fungal peptides derived from domain III of
XX bactericidal/permeability-increasing protein useful for killing or
PT inhibiting replication of fungi and for treating fungal infections -
XX Example 2; Columns 205-206; 134pp; English.
PS

XX The present invention relates to antifungal peptides (see
CC AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C.albicans, C.glabrata, C.krusei,
CC C.lusitanae, C.parapsilosis and C.tropicalis.
XX
SQ Sequence 9 AA;

Query Match 89.6%; Score 43; DB 22; Length 9;
Best Local Similarity 88.9%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLQLLWKK 9
Db 1 KKLQIAWKK 9
11111111;

RESULT 11
AAO00543
ID AAO00543 standard; Protein; 128 AA.
XX
AC AAO00543;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 14435.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI80474.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 14435; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and

CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 128 AA;

Query Match 79.2%; Score 38; DB 22; Length 128;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
Db 58 KMQLLWKK 66
11111111;

RESULT 12
ABG65564
ID ABG65564 standard; Protein; 325 AA.
XX
AC ABG65564;
XX
DT 23-AUG-2002 (first entry)
XX
DE Human breast specific polypeptide, BSP #34.
XX
KW Human; breast specific protein; BSP; breast cancer; vaccine;
KW mammary tumour; cytostatic; gene therapy; non-cancerous breast disorder.
XX
OS Homo sapiens.
XX
PN WO200236807-A2.
XX
PD 10-MAY-2002.
XX
PF 29-OCT-2001; 2001WO-US46888.
XX
PR 27-OCT-2000; 2000US-243802P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Sun Y, Recipon H, Salceda S, Liu C, Turner LR;
XX
DR WPI; 2002-463415/49.
XX
PT New breast-specific nucleic acids and polypeptides, useful for
PT identifying, diagnosing, monitoring, staging, imaging, and treating
PT breast cancer and non-cancerous disease states in breast tissues -
XX
PS Claim 11; Page 231-232; 281pp; English.
XX
CC The invention relates to breast specific nucleic acids (BSNA) and
CC breast-specific polypeptides (BSP). Also included are a method for
CC determining the BSNA in a sample, a vector comprising a BSNA, a host cell
CC comprising the vector, a method for producing a polypeptide encoded
CC by a BSNA, an anti-BSP antibody and a method for determining the presence
CC of a BSP in a sample. The breast-specific nucleic acids, polypeptides and
CC compositions comprising them are useful for identifying, diagnosing,
CC monitoring, staging, imaging, and treating breast cancer, mammary tumour
CC and non-cancerous disease states in breast tissue; for identifying breast
CC tissue; for monitoring, identifying and/or designing agonists and
CC antagonists of the polypeptides; in gene therapy; in producing transgenic
CC animals and cells; for producing engineered breast tissue for treatment
CC and research; and as elements in an array or computer program for pattern
CC recognition of breast disorders. The nucleic acids may be used as
CC hybridisation probes to detect, characterise and quantify hybridising
CC nucleic acids in, and isolate hybridising nucleic acids from, both
CC genomic and transcript-derived nucleic acid samples. The BSP
CC protein may be used in a vaccine composition for raising an immune
CC response against breast cancer. The present sequence is BSP protein of
CC the invention.
XX
SQ Sequence 325 AA;

Query Match 79.2%; Score 38; DB 23; Length 325;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKLQILWKK 9
|:::|
Db 78 KKLQILWKK 85

RESULT 13
ABG15487
ID ABG15487 standard; Protein; 369 AA.
XX
AC ABG15487;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #15478.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS79674.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 45846; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 369 AA;

Query Match 79.2%; Score 38; DB 22; Length 369;

Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
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Db 172 KKLQILWKK 180

RESULT 14
ABG15486
ID ABG15486 standard; Protein; 414 AA.
XX
AC ABG15486;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #15477.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS79673.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 45845; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 414 AA;

Query Match 79.2%; Score 38; DB 22; Length 414;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLQILWKK 9
|:::|||||
Db 310 KQMRILWKK 318

Search completed: October 14, 2003, 14:41:32
Job time : 39.7917 secs

RESULT 15
ABB05745
ID ABB05745 standard; Protein; 547 AA.
XX AC ABB05745;
XX DT 01-MAY-2002 (first entry)
XX DE Mouse zcytor17 protein SEQ ID NO:93.
XX KW zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW inflammatory disease; pancreatitis; inflammatory bowel disease.
XX OS Mus musculus.
XX PN WO200200721-A2.
XX PD 03-JAN-2002.
XX PF 26-JUN-2001; 2001WO-US20484.
XX PR 26-JUN-2000; 2000US-214282P.
XX PR 29-JUN-2000; 2000US-214955P.
XX PR 08-FEB-2001; 2001US-267963P.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;
PI Maurer MF;
XX DR WPI; 2002-090519/12.
XX DR N-PSDB; ABA93843.
XX PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT splenic, blood or bone disorders -
XX Example 21; Page 233-235; 235pp; English.
XX CC The present invention describes a cytokine receptor designated zcytor17.
CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
CC antirheumatic, antiarthritic and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. Agonists or
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
CC immunity and for stimulating lymphocyte proliferation, such as in the
CC treatment of infections involving immunosuppression, including certain
CC viral infections. They are also useful for inducing cytotoxicity and
CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC pancreatitis, and inflammatory bowel disease. zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC exemplification of the present invention.

SQ Sequence 547 AA;
Query Match 75.0%; Score 36; DB 23; Length 547;
Best Local Similarity 55.6%; Pred. NO. 4.5e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:23 ; Search time 12.75 Seconds
(without alignments)
29.866 Million cell updates/sec

Title: US-09-881-490-163
Perfect score: 48
Sequence: 1 KKLQILWKK 9

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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 48 | 100.0 | 9 | 2 | US-08-621-259A-163 |
| 2 | 48 | 100.0 | 9 | 5 | PCT-US95-09262-163 |
| 3 | 43 | 89.6 | 8 | 2 | US-08-621-259A-205 |
| 4 | 43 | 89.6 | 9 | 2 | US-08-621-259A-207 |
| 5 | 35 | 72.9 | 303 | 4 | US-09-205-258-818 |
| 6 | 35 | 72.9 | 400 | 4 | US-09-205-258-822 |
| 7 | 35 | 72.9 | 453 | 4 | US-09-252-991A-31268 |
| 8 | 34 | 70.8 | 18 | 4 | US-09-450-315A-1 |
| 9 | 34 | 70.8 | 20 | 4 | US-09-000-692-1 |
| 10 | 34 | 70.8 | 281 | 4 | US-09-107-532A-6750 |
| 11 | 33 | 68.8 | 9 | 2 | US-08-621-803-220 |
| 12 | 33 | 68.8 | 9 | 2 | US-08-621-259A-212 |
| 13 | 33 | 68.8 | 9 | 3 | US-09-217-352-220 |
| 14 | 33 | 68.8 | 10 | 2 | US-08-621-259A-198 |
| 15 | 33 | 68.8 | 10 | 2 | US-08-621-259A-199 |
| 16 | 33 | 68.8 | 10 | 5 | PCT-US95-09262-198 |
| 17 | 33 | 68.8 | 10 | 5 | PCT-US95-09262-199 |
| 18 | 33 | 68.8 | 358 | 4 | US-09-328-352-7579 |
| 19 | 33 | 68.8 | 822 | 4 | US-09-198-452A-956 |
| 20 | 32 | 66.7 | 33 | 2 | US-08-653-632-63 |
| 21 | 32 | 66.7 | 33 | 4 | US-09-194-296-6 |
| 22 | 32 | 66.7 | 644 | 4 | US-09-107-532A-7277 |
| 23 | 32 | 66.7 | 1095 | 4 | US-09-107-532A-3855 |
| 24 | 32 | 66.7 | 1464 | 3 | US-09-045-360-2 |
| 25 | 31 | 64.6 | 96 | 4 | US-09-227-357-159 |
| 26 | 31 | 64.6 | 185 | 4 | US-09-529-157-6 |
| 27 | 31 | 64.6 | 185 | 4 | US-09-529-157-7 |

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| 28 | 31 | 64.6 | 221 | 4 | US-09-495-406-23 | Sequence 23, Appl |
| 29 | 31 | 64.6 | 240 | 4 | US-09-107-532A-4551 | Sequence 4551, Ap |
| 30 | 31 | 64.6 | 255 | 2 | US-08-933-750C-7 | Sequence 7, Appli |
| 31 | 31 | 64.6 | 255 | 3 | US-09-234-613-7 | Sequence 7, Appli |
| 32 | 31 | 64.6 | 388 | 1 | US-08-429-742-4 | Sequence 4, Appli |
| 33 | 31 | 64.6 | 415 | 3 | US-08-861-774E-26 | Sequence 26, Appl |
| 34 | 31 | 64.6 | 518 | 3 | US-09-045-360-4 | Sequence 4, Appli |
| 35 | 31 | 64.6 | 686 | 4 | US-09-653-839-8 | Sequence 8, Appli |
| 36 | 31 | 64.6 | 702 | 4 | US-09-653-839-6 | Sequence 6, Appli |
| 37 | 31 | 64.6 | 723 | 4 | US-09-653-839-4 | Sequence 4, Appli |
| 38 | 31 | 64.6 | 739 | 4 | US-09-653-839-2 | Sequence 2, Appli |
| 39 | 31 | 64.6 | 1064 | 3 | US-08-726-214-8 | Sequence 8, Appli |
| 40 | 31 | 64.6 | 1077 | 4 | US-09-412-210-1 | Sequence 1, Appli |
| 41 | 31 | 64.6 | 1167 | 3 | US-08-857-076-48 | Sequence 48, Appl |
| 42 | 30 | 62.5 | 14 | 1 | US-08-311-611A-106 | Sequence 106, App |
| 43 | 30 | 62.5 | 14 | 1 | US-08-372-783-106 | Sequence 106, App |
| 44 | 30 | 62.5 | 14 | 1 | US-08-372-105-106 | Sequence 106, App |
| 45 | 30 | 62.5 | 14 | 1 | US-08-306-473A-106 | Sequence 106, App |

ALIGNMENTS

RESULT 1
US-08-621-259A-163
; Sequence 163, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.332"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1-9
; OTHER INFORMATION: /label= D-Amino Acids
; OTHER INFORMATION: /note= "Positions 1-9 are D-amino acids"

KEY: Modified-site
ION: C-Terminus
R INFORMATION: /label= Amidation
R INFORMATION: /note= "The C-Terminus is Amidated."
59A-163

.ch 100.0%; Score 48; DB 2: Length 9;
al Similarity 100.0%; Pred. No. 2.5e+05;
9: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KKLQILWKK 9
1 KKLQILWKK 9

39262-163
e 163, Application PC/TUS9509262
L INFORMATION:
ICANT:
E OF INVENTION: Anti-Fungal Peptides
ER OF SEQUENCES: 206
ESPONDECE ADDRESS:
DRESSEE: Marshall, O'Toole, Gerstein, Murray & Horun
REF: 6300 Sears Tower, 233 South Wacker Drive
ITY: Chicago
TATE: Illinois
COUNTRY: United States of America
IP: 60606-6402
PUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
RRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09262
FILING DATE:
ROR APPLICATION DATA:
APPLICATION NUMBER: 08/372,105
FILING DATE: 13-JAN-95
ROR APPLICATION DATA:
APPLICATION NUMBER: 08/306,473
FILING DATE: 15-SEP-94
ROR APPLICATION DATA:
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-94
ROR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-94
ROR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-94
ROR APPLICATION DATA:
APPLICATION NUMBER: 08/093,202
FILING DATE: 15-JUL-93
ROR APPLICATION DATA:
APPLICATION NUMBER: 08/030,544
FILING DATE: 12-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/10040
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 163:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: "XMP.332"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-9
OTHER INFORMATION: /label= D-Amino Acids
OTHER INFORMATION: /note= "Positions 1-9 are D-amino acids"
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LOCATION: C-Terminus
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OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-163

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Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
Db 1 KKLQILWKK 9

RESULT 3
US-08-621-259A-205
Sequence 205, Application US/08621259A
Patent No. 5858974
GENERAL INFORMATION:
APPLICANT: Little II, Roger G
APPLICANT: Lim, Edward
APPLICANT: Fadem, Mitchell B.
TITLE OF INVENTION: Anti-Fungal Peptides
NUMBER OF SEQUENCES: 252
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,259A
FILING DATE: 21-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/504,841
FILING DATE: 20-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11021US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX:
INFORMATION FOR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: "XMP.374"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation

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; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1-8
; OTHER INFORMATION: /label= D-Amino Acids
; OTHER INFORMATION: /note= "Positions 1-8 are D-Amino Acids."
US-08-621-259A-205

Query Match      89.6%; Score 43; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KKLQILWKK 9
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Db      1 KKLQILWKK 8

RESULT 4
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; Sequence 207, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Mailloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 207:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: "XMP.376"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1-9
; OTHER INFORMATION: /label= D-Amino Acids
; OTHER INFORMATION: /note= "Positions 1-9 are D-Amino Acids."
S-08-621-259A-207
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Query Match      89.6%; Score 43; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2.5e+05;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KKLQILWKK 9
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Db      1 KKLQIAWKK 9

RESULT 5
US-09-205-258-818
; Sequence 818, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 818
LENGTH: 303
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-818

Query Match 72.9%; Score 35; DH 4; Length 303;
Best Local Similarity 75.0%; Pred. No. 1.3e-02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWK 8
Db 199 QQLQILWK 206

RESULT 6

US-09-205-258-822
Sequence 822, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 822
LENGTH: 400
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-822

Query Match 72.9%; Score 35; DB 4; Length 400;
Best Local Similarity 75.0%; Pred. No. 1.7e-02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLOIILWK 8
: : : : :
Db 199 OOLQILWK 206

RESULT 7

US-09-252-991A-31268
; Sequence 31268, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31268
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31268

Query Match 72.9%; Score 35; DB 4; Length 453;

Best Local Similarity 66.7%; Pred. No. 1.9e+02;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKLOIILWK 9
: : : : :
Db 158 KKLQEIWEK 166

RESULT 8

US-09-450-315A-1
; Sequence 1, Application US/09450315A
; Patent No. 6379966

; GENERAL INFORMATION:

; APPLICANT: WOLFF, JON A
; APPLICANT: Monahan, Sean D
; APPLICANT: Slattum, Paul M
; APPLICANT: Hagstrom, James E
; APPLICANT: Budker, Vladimir G
; APPLICANT: Rozema, David B
; TITLE OF INVENTION: INTRAVASCULAR DELIVERY OF NON-VIRAL NUCLEIC ACID
; FILE REFERENCE: Mirus.013.03
; CURRENT APPLICATION NUMBER: US/09/450.315A
; CURRENT FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 60/121730
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/146564
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
; OTHER INFORMATION: amphipathic peptide with alternating hydrophilic
; OTHER INFORMATION: and hydrophobic residues.
US-09-450-315A-1

Query Match 70.8%; Score 34; DB 4; Length 18;

Best Local Similarity 77.8%; Pred. No. 15;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKLOIILWK 9
: : : : :
Db 199 OOLQILWK 206

Db 4 KKLKLLWK 12

RESULT 9

US-09-000-692-1
; Sequence 1, Application US/09000692
; Patent No. 6339067

; GENERAL INFORMATION:

; APPLICANT: WOLFF, JON A
; APPLICANT: HAGSTROM, JAMES E
; APPLICANT: BUDKER, VLADIMIR G
; APPLICANT: TRUBETSKOY, VLADIMIR S
; APPLICANT: SLATTUM, PAUL M
; APPLICANT: HANSON, LISA J
; TITLE OF INVENTION: A PROCESS OF MAKING A COMPOUND BY FORMING A POLYMER
; TITLE OF INVENTION: FROM A TEMPLATE DRUG
; FILE REFERENCE: TPCIP000692
; CURRENT APPLICATION NUMBER: US/09/000,692
; CURRENT FILING DATE: 1997-12-30
; EARLIER APPLICATION NUMBER: 08/778657
; EARLIER FILING DATE: 1997-01-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: AMPHIPATHIC
US-09-000-692-1

Query Match 70.8%; Score 34; DB 4; Length 20;

Best Local Similarity 77.8%; Pred. No. 17;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKLOIILWK 9
: : : : :
Db 5 KKLKLLWK 13

RESULT 10

US-09-107-532A-6750
; Sequence 6750, Application US/09107532A
; Patent No. 6583275

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6750:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...281
; SEQUENCE DESCRIPTION: SEQ ID NO: 6750:
US-09-107-532A-6750
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; Query Match 70.8%; Score 34; DB 4; Length 281;
; Best Local Similarity 55.6%; Pred. No. 1.8e+02;
; Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 KKLQILWKK 9
; Db 27 QKVQVLWPK 35
;
; RESULT 11
; US-08-621-803-220
; Sequence 220, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.381"
; FRATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
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US-08-621-803-220
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; Query Match 68.8%; Score 33; DB 2; Length 9;
; Best Local Similarity 77.8%; Pred. No. 2.5e+05;
; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 KKLQILWKK 9
; Db 1 KKLQILLKK 9
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; RESULT 12
; US-08-621-259A-212
; Sequence 212, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 110210S02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 212:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.381"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-212
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; Query Match 68.8%; Score 33; DB 2; Length 9;
; Best Local Similarity 77.8%; Pred. No. 2.5e+05;
; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 KKLQILWKK 9
; Db 1 KKLQILLKK 9
;
; RESULT 13
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US-09-217-352-220
; Sequence 220, Application US/09217352
; Patent No. 6274344
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,352
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.381"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-09-217-352-220
Query Match 68.8%; Score 33; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 2.5e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLQLLWKK 9
Db 1 KKLQLLWKK 9
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RESULT 14
US-08-621-259A-198
; Sequence 198, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
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STATE: Illinois
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,259A
FILING DATE: 21-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/504,841
FILING DATE: 20-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11021US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX:
INFORMATION FOR SEQ ID NO: 198:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.367"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-10
OTHER INFORMATION: /label= D-Amino Acids
OTHER INFORMATION: /note= "Positions 1-10 are D-amino acids"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-198
Query Match 68.8%; Score 33; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LQILWK 8
Db 5 LQILWK 10
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RESULT 15
US-08-621-259A-199
; Sequence 199, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 199:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.368"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetylated
; OTHER INFORMATION: /note= "Position 1 is acetylated."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1-10
; OTHER INFORMATION: /label= D-Amino Acids
; OTHER INFORMATION: /note= "Positions 1-10 are D-amino acids"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-199
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Query Match          68.8%  Score 33; DB 2: Length 10;
Best Local Similarity 100.0%; Pred. NO. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      3 LQILWK 8
        |||||
Db      5 LQILWK 10
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Search completed: October 14, 2003, 14:42:46
Job time : 13.75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:34:14 ; Search time 21.9375 seconds
(without alignments)
66.104 Million cell updates/sec

Title: US-09-881-490-163
Perfect score: 48
Sequence: 1 KKLQIIWKK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA.*

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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US50_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------------------|-------------------|
| 1 | 48 | 100.0 | 9 | 9 US-09-881-490-163 | Sequence 163, App |
| 2 | 38 | 79.2 | 325 | 15 US-10-082-830-193 | Sequence 193, App |
| 3 | 36 | 75.0 | 547 | 11 US-09-892-949-93 | Sequence 93, Appl |
| 4 | 36 | 75.0 | 662 | 11 US-09-892-949-57 | Sequence 57, Appl |
| 5 | 36 | 75.0 | 726 | 11 US-09-972-708-12 | Sequence 12, Appl |
| 6 | 35 | 72.9 | 231 | 12 US-10-107-857-48 | Sequence 48, Appl |
| 7 | 35 | 72.9 | 303 | 12 US-09-933-767-818 | Sequence 818, App |
| 8 | 35 | 72.9 | 303 | 15 US-10-023-282-818 | Sequence 818, App |
| 9 | 35 | 72.9 | 400 | 15 US-09-933-767-822 | Sequence 822, App |
| 10 | 35 | 72.9 | 400 | 15 US-10-023-282-822 | Sequence 822, App |
| 11 | 35 | 72.9 | 738 | 12 US-10-175-270-2 | Sequence 2, Appli |
| 12 | 35 | 72.9 | 738 | 12 US-10-107-857-30 | Sequence 30, Appl |
| 13 | 35 | 72.9 | 740 | 12 US-10-325-430-15 | Sequence 15, Appl |
| 14 | 35 | 72.9 | 795 | 12 US-10-107-857-21 | Sequence 21, Appl |
| 15 | 35 | 72.9 | 855 | 12 US-10-107-857-45 | Sequence 45, Appl |

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| 16 | 34 | 70.8 | 18 | 9 | US-09-447-966-1 | Sequence 1, Appli |
| 17 | 34 | 70.8 | 18 | 12 | US-10-085-378-2 | Sequence 2, Appli |
| 18 | 34 | 70.8 | 49 | 9 | US-09-864-761-41571 | Sequence 41571, A |
| 19 | 34 | 70.8 | 560 | 10 | US-09-978-295A-420 | Sequence 420, App |
| 20 | 34 | 70.8 | 560 | 10 | US-09-978-697-420 | Sequence 420, App |
| 21 | 34 | 70.8 | 560 | 10 | US-09-978-392A-420 | Sequence 420, App |
| 22 | 34 | 70.8 | 560 | 10 | US-09-999-832A-420 | Sequence 420, App |
| 23 | 34 | 70.8 | 560 | 11 | US-09-978-189-420 | Sequence 420, App |
| 24 | 34 | 70.8 | 560 | 11 | US-09-978-608A-420 | Sequence 420, App |
| 25 | 34 | 70.8 | 560 | 11 | US-09-978-585A-420 | Sequence 420, App |
| 26 | 34 | 70.8 | 560 | 11 | US-09-978-191A-420 | Sequence 420, App |
| 27 | 34 | 70.8 | 560 | 11 | US-09-978-403A-420 | Sequence 420, App |
| 28 | 34 | 70.8 | 560 | 11 | US-09-978-564A-420 | Sequence 420, App |
| 29 | 34 | 70.8 | 560 | 11 | US-09-999-833A-420 | Sequence 420, App |
| 30 | 34 | 70.8 | 560 | 11 | US-09-981-915A-420 | Sequence 420, App |
| 31 | 34 | 70.8 | 560 | 11 | US-09-978-824-420 | Sequence 420, App |
| 32 | 34 | 70.8 | 560 | 11 | US-09-918-585A-420 | Sequence 420, App |
| 33 | 34 | 70.8 | 560 | 11 | US-09-978-423A-420 | Sequence 420, App |
| 34 | 34 | 70.8 | 560 | 11 | US-09-978-193A-420 | Sequence 420, App |
| 35 | 34 | 70.8 | 560 | 11 | US-09-999-830A-420 | Sequence 420, App |
| 36 | 34 | 70.8 | 560 | 11 | US-09-978-757A-420 | Sequence 420, App |
| 37 | 34 | 70.8 | 560 | 11 | US-09-978-187B-420 | Sequence 420, App |
| 38 | 34 | 70.8 | 560 | 11 | US-09-978-643A-420 | Sequence 420, App |
| 39 | 34 | 70.8 | 560 | 12 | US-09-978-375A-420 | Sequence 420, App |
| 40 | 34 | 70.8 | 560 | 12 | US-09-978-188A-420 | Sequence 420, App |
| 41 | 34 | 70.8 | 560 | 12 | US-09-978-298A-420 | Sequence 420, App |
| 42 | 34 | 70.8 | 560 | 12 | US-10-143-031A-420 | Sequence 420, App |
| 43 | 34 | 70.8 | 560 | 12 | US-10-002-967A-420 | Sequence 420, App |
| 44 | 34 | 70.8 | 560 | 12 | US-10-017-083A-420 | Sequence 420, App |
| 45 | 34 | 70.8 | 560 | 12 | US-10-143-030A-420 | Sequence 420, App |

ALIGNMENTS

RESULT 1

US-09-881-490-163
; Sequence 163, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94

APPLICATION NUMBER: 08/093,202
FILING DATE: 15-JUL-93
APPLICATION NUMBER: 08/030,644
FILING DATE: 12-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 100-238/11021US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 163:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.332"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-9
OTHER INFORMATION: /label= D-Amino Acids
/note= "Positions 1-9 are D-amino acids"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
/note= "The C-terminus is Amidated"
SEQUENCE DESCRIPTION: SEQ ID NO: 163:
US-09-881-490-163

Query Match 100.0%; Score 48; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
|:|:|:|:|
Db 1 KKLQILWKK 9

RESULT 2
US-10-082-830-193
; Sequence 193, Application US/10082830
; Publication No. US20030077604A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Hervé
; APPLICANT: Salceda, Susana
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
; FILE REFERENCE: DEX-0249
; CURRENT APPLICATION NUMBER: US/10/082,830
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,802
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 282
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 193
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-082-830-193

Query Match 79.2%; Score 38; DB 15; Length 325;
Best Local Similarity 75.0%; Pred. No. 98;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKLQILWKK 9

Db 78 KQLVWKK 85
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RESULT 3
US-09-892-949-93
; Sequence 93, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 93
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-892-949-93

Query Match 75.0%; Score 36; DB 11; Length 547;
Best Local Similarity 55.6%; Pred. No. 3.2e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
|:|:|:|:|
Db 258 RKVRLWKK 266

RESULT 4
US-09-892-949-57
; Sequence 57, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
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; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 662
; TYPE: PRT
; ORGANISM: mus musculus
US-09-892-949-57

Query Match 75.0%; Score 36; DB 11; Length 662;
Best Local Similarity 55.6%; Pred. No. 3.8e+02;

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Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLQILWKK 9
Db 258 RKVRLWKK 266
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RESULT 5
US-09-972-708-12
; Sequence 12, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: DuBose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-972-708-12
Query Match 75.0%; Score 36; DB 11; Length 726;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLQILWKK 9
Db 241 RKVRLWKK 249
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RESULT 6
US-10-107-857-48
; Sequence 48, Application JS/10107857
; Publication No. US20030170784A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 07334-251001
; CURRENT APPLICATION NUMBER: US/10/107,857
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/514,009
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-857-48
Query Match 72.9%; Score 35; DB 12; Length 231;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLQILWKK 8
Db 127 QQLQILWKK 134
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RESULT 7
US-09-933-767-818
; Sequence 818, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1997-12-18
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; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 818
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-933-767-818

Query Match 72.9%; Score 35; DB 12; Length 303;
Best Local Similarity 75.0%; Pred. NC. 2.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWK 8
Db 199 QQLQILWK 206

RESULT 8
US-10-023-282-818
; Sequence 818, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/023,282
; CURRENT FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: 09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04

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; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923

EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 818
LENGTH: 303
TYPE: PRT
ORGANISM: Homo sapiens
US-10-023-282-818

Query Match 72.9% Score 35; DB 15; Length 303;
Best Local Similarity 75.0%; Pred. NO. 2.8e-02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KKLQILWK 8
Db 199 QQLQILWK 206

RESULT 9

US-09-933-767-822
Sequence 822, Application US/09933767
Publication No. US20030181692A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P2
CURRENT APPLICATION NUMBER: US/09/933,767
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: PCT/US01/05614
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/184,836
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/193,170
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/205,258
PRIOR FILING DATE: 1998-12-04
PRIOR APPLICATION NUMBER: PCT/US98/11422
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/048,885
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,375
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,881
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,880
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,896
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,020
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,876
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,895
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,884
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,894
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,971
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,964
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,882
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,899
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,893
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,900

PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,901
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,892
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,915
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,019
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,972
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,916
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,373
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,875
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,374
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,917
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PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,877
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,878
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/068,054
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,064
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,053
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/070,923
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/073,160
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,159
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,165
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,164
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/085,925
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,921
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,923
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,922
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/094,657
NUMBER OF SEQ ID NOS: 1245
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 822
LENGTH: 400

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-933-767-822

Query Match      72.9%; Score 35; DB 12; Length 400;
Best Local Similarity 75.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLQILWK 8
       ::::|||||
Db      199 QQLQILWK 206

RESULT 10
US-10-023-282-822
; Sequence 822, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/023,282
; CURRENT FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: 09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
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; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
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; EARLIER APPLICATION NUMBER: 60/048,972
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; EARLIER APPLICATION NUMBER: 60/049,373
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; EARLIER APPLICATION NUMBER: 60/048,917
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 822
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-282-822

Query Match      72.9%; Score 35; DB 15; Length 400;
Best Local Similarity 75.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLQILWK 8
       ::::|||||
Db      199 QQLQILWK 206

RESULT 11
US-10-175-270-2
; Sequence 2, Application US/10175270
; Publication No. US20030166548A1
; GENERAL INFORMATION:
; APPLICANT: PETERSON, JOHNNY W.
; APPLICANT: SAINI, SHAMSHER S.
; APPLICANT: WOOD, THOMAS G.
; APPLICANT: CHOPRA, ASHOK K.
; TITLE OF INVENTION: ANTI-INFLAMMATORY AND OTHER THERAPEUTIC PROPHYLACTIC OR DIAGN
; TITLE OF INVENTION: SYNTHETIC MELITTIN AND NE
; TITLE OF INVENTION: W RELATED PEPTIDES
; FILE REFERENCE: UTSG:213
; CURRENT APPLICATION NUMBER: US/10/175,270
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/458,397
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: PCT/US98/12340
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 738
; TYPE: PRT
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; ORGANISM: Human
US-10-175-270-2

Query Match          72.9%; Score 35; DB 12; Length 738;
Best Local Similarity 75.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLQILWK 8
Db      537 QQLQILWK 544

RESULT 12
US-10-107-857-30
; Sequence 30, Application US/10107857
; Publication No. US20030170784A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 07334-251001
; CURRENT APPLICATION NUMBER: US/10/107,857
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/514,009
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-857-30

Query Match          72.9%; Score 35; DB 12; Length 738;
Best Local Similarity 75.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLQILWK 8
Db      537 QQLQILWK 544

RESULT 13
US-10-325-430-15
; Sequence 15, Application US/10325430
; Publication No. US20030153525A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Rosenfeld, Julie Beth
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
; TITLE OF INVENTION: 32838,336 and 52908
; FILE REFERENCE: MP101-294PIRNM
; CURRENT APPLICATION NUMBER: US/10/325,430
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/341,953
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 740
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-325-430-15

Query Match          72.9%; Score 35; DB 12; Length 740;
Best Local Similarity 66.7%; Pred. No. 6.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 KKLQILWK 9
Db      84 KKIQTQWK 92

; ORGANISM: Human
US-10-175-270-2

Query Match          72.9%; Score 35; DB 12; Length 738;
Best Local Similarity 75.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLQILWK 8
Db      537 QQLQILWK 544

RESULT 14
US-10-107-857-21
; Sequence 21, Application US/10107857
; Publication No. US20030170784A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 07334-251001
; CURRENT APPLICATION NUMBER: US/10/107,857
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/514,009
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 795
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-857-21

Query Match          72.9%; Score 35; DB 12; Length 795;
Best Local Similarity 75.0%; Pred. No. 6.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLQILWK 8
Db      594 QQLQILWK 601

RESULT 15
US-10-107-857-45
; Sequence 45, Application US/10107857
; Publication No. US20030170784A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 07334-251001
; CURRENT APPLICATION NUMBER: US/10/107,857
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/514,009
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-857-45

Query Match          72.9%; Score 35; DB 12; Length 855;
Best Local Similarity 75.0%; Pred. No. 6.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLQILWK 8
Db      654 QQLQILWK 661

Search completed: October 14, 2003, 14:44:51
Job time : 23.9375 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw mode!

Run on: October 14, 2003, 14:33:18 ; Search time 11.8125 Seconds
(without alignments)
73.272 Million cell updates/sec

Title: US-09-881-490-163
Perfect score: 48
Sequence: 1 KKLQILWKK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|------------|-------|-------|--------|----|--------|--------------------|
| 1 | 39 | 81.2 | 339 | 1 | R6BY13 | ribosomal protein |
| 2 | 39 | 81.2 | 1273 | 2 | T38292 | hypothetical prote |
| 3 | 35 | 72.9 | 326 | 2 | T24391 | hypothetical prote |
| 4 | 35 | 72.9 | 588 | 2 | D70394 | mannosyltransferas |
| 5 | 35 | 72.9 | 795 | 2 | T43447 | hypothetical prote |
| 6 | 35 | 72.9 | 867 | 2 | JH0225 | L96 protein - Tipu |
| 7 | 35 | 72.9 | 2925 | 2 | TC0133 | RNA-directed RNA p |
| 8 | 34 | 70.8 | 137 | 2 | D86439 | protein T19E23.15 |
| 9 | 34 | 70.8 | 157 | 1 | W6WLB5 | E6 protein - human |
| 10 | 34 | 70.8 | 205 | 2 | H72277 | phosphoribosylglyc |
| 11 | 34 | 70.8 | 308 | 2 | H86397 | protein T7N9.8 (im |
| 12 | 34 | 70.8 | 424 | 1 | B64216 | hemolysin tlyc hom |
| 13 | 34 | 70.8 | 451 | 2 | T19491 | hypothetical prote |
| 14 | 34 | 70.8 | 647 | 2 | JC4239 | phospholipase A2-a |
| 15 | 34 | 70.8 | 1042 | 2 | S76045 | hypothetical prote |
| 16 | 33 | 68.8 | 142 | 2 | S36509 | E6 protein - human |
| 17 | 33 | 68.8 | 156 | 1 | W6WL47 | E6 protein - human |
| 18 | 33 | 68.8 | 243 | 2 | AD3405 | transcription regu |
| 19 | 33 | 68.8 | 263 | 2 | G81272 | hypothetical prote |
| 20 | 33 | 68.8 | 313 | 2 | A69496 | TPR domain-contain |
| 21 | 33 | 68.8 | 394 | 2 | E81286 | probable polysacch |
| 22 | 33 | 68.8 | 412 | 2 | B97077 | diverged AAA-famil |
| 23 | 33 | 68.8 | 413 | 2 | T12533 | hypothetical prote |
| 24 | 33 | 68.8 | 476 | 2 | C87454 | PQQ enzyme repeat |
| 25 | 33 | 68.8 | 502 | 1 | A41361 | serine/threonine-s |
| 26 | 33 | 68.8 | 513 | 1 | A47436 | 1,25-dihydroxyvita |
| 27 | 33 | 68.8 | 513 | 1 | S60303 | serine/threonine-s |
| 28 | 33 | 68.8 | 513 | 1 | S60304 | serine/threonine-s |
| 29 | 33 | 68.8 | 514 | 2 | H97819 | hypothetical prote |

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|----|------|------|------|---|--------|--------------------|
| 30 | 33 | 68.8 | 541 | 2 | T25258 | hypothetical prote |
| 31 | 33 | 68.8 | 563 | 2 | T27313 | hypothetical prote |
| 32 | 33 | 68.8 | 578 | 2 | A35810 | alpha,alpha-trehal |
| 33 | 33 | 68.8 | 610 | 2 | T25262 | hypothetical prote |
| 34 | 33 | 68.8 | 625 | 2 | AD2251 | two-component sens |
| 35 | 33 | 68.8 | 803 | 2 | F59433 | RhoGAP protein (im |
| 36 | 33 | 68.8 | 818 | 2 | A59433 | KIAA0672 protein I |
| 37 | 33 | 68.8 | 822 | 2 | C72023 | chltr probable pho |
| 38 | 33 | 68.8 | 822 | 2 | B81518 | conserved hypothet |
| 39 | 33 | 68.8 | 822 | 2 | E86601 | CHLTR probable pho |
| 40 | 33 | 68.8 | 890 | 2 | C96654 | hypothetical prote |
| 41 | 33 | 68.8 | 990 | 2 | T16554 | hypothetical prote |
| 42 | 33 | 68.8 | 2628 | 2 | S59413 | probable membrane |
| 43 | 33 | 68.8 | 3351 | 2 | T13812 | lipophorin - fruit |
| 44 | 32.5 | 67.7 | 145 | 2 | E70168 | flagellar protein |
| 45 | 32.5 | 67.7 | 665 | 2 | E90351 | ATP-dependent heli |

ALIGNMENTS

RESULT 1

R6BY13
ribosomal protein MRP13 precursor, mitochondrial - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein G4618; protein YGR084c; ribosomal protein YMS-A
C;Species: Saccharomyces cerevisiae
C;Date: 30-Jun-1992 #sequence_revision 19-Jul-1996 #text_change 16-Jun-2000
C;Accession: S64379; A30237; S78035; S07831
R;Wedler, H.; Scharfe, M.; Wedler, E.; Wambutt, R.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64356
A;Accession: S64379
A;Molecule type: DNA
A;Residues: 1-339 <WED>
A;Cross-references: EMBL:Z72869; NID:gl323120; PIDN:CAA97086.1; PID:gl323121; GSPDB:G
A;Experimental source: strain S288C
R;Partaledis, J.A.; Mason, T.L.
Mol. Cell. Biol. 8, 3647-3660, 1988
A;Title: Structure and regulation of a nuclear gene in Saccharomyces cerevisiae that
A;Reference number: A30237; MUID:89127203; PMID:3065621
A;Accession: A30237
A;Molecule type: DNA
A;Residues: 28-113, 'S', 115-309, 'RIQRSIRHAFESV', 323, 'TVGNTLSGSG', 336, 'RG', 339, 'IVQNTHR
A;Cross-references: EMBL:M22109; NID:gl71970; PIDN:AAA34788.1; PID:gl71971
A;Note: the authors translated the codon AGT for residues 4, 227, 236, and 282 as Phe
R;Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wit
Eur. J. Biochem. 245, 449-456, 1997
A;Title: Identification and characterization of the genes for mitochondrial ribosomal
A;Reference number: S78018; MUID:97296414; PMID:9151978
A;Accession: S78035
A;Molecule type: protein
A;Residues: 'X', 39-51 <KIT>
C;Genetics:
A;Gene: SGD:MRP13; MIPS:YGR084C
A;Cross-references: SGD:S0003316; MIPS:YGR084C
A;Map position: 7R
A;Genome: nuclear
C;Superfamily: Saccharomyces cerevisiae mitochondrial ribosomal protein MRP13
C;Keywords: mitochondrion; protein biosynthesis; ribosome
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F:48-339/Product: ribosomal protein MRP13 #status predicted <MAT>

Query Match 81.2%; Score 39; DB 1; Length 339;
Best Local Similarity 66.7%; Pred. NO. 9.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KKLQILWKK 9

Db 209 RKLQVAVKK 217

RESULT 2

T38292

hypothetical protein SPAC23E2.02 - fission yeast (Schizosaccharomyces pombe);
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38292
R:Skelton, J.; Church, C.M.; Barrell, B.G.; Rajandream, M.A.; Waish, S.V.
submitted to the EMBL Data Library, January 1996
A:Reference number: Z21784
A:Accession: T38292
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1273 <SKE>
A:Cross-references: EMBL:Z68887; PIDN:CAA93114.1; GSPDB:GN00066; SPDB:SPAC23E2.02
A:Experimental source: strain 972h-; cosmid c23E2
C:Genetics:
A:Gene: SPDB:SPAC23E2.02
A:Map position: 1
A:Introns: 8/2; 862/3

Query Match 81.2%; Score 39; DB 2; Length 1273;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
||| ||| ||
Db 657 KKLNLWEK 665

RESULT 3
T24391
hypothetical protein T03E6.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T24391
R:Lloyd, C.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19885
A:Accession: T24391
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-326 <WII>
A:Cross-references: EMBL:Z92812; PIDN:CAH07279.1; GSPDB:GN00023; CESP:T03E6.5
A:Experimental source: clone T03E6
C:Genetics:
A:Gene: CESP:T03E6.5
A:Map position: 5
A:Introns: 99/1; 160/3; 236/3
C:Superfamily: Caenorhabditis hypothetical protein C49G7.2

Query Match 72.9%; Score 35; DB 2; Length 326;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILW 7
: |||||
Db 300 RKLQILW 306

RESULT 4
D70394
mannosyltransferase A - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C:Accession: D70394
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: D70394
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-588 <AQF>
A:Cross-references: GB:AE000723; NID:q2983569; PIDN:AAC07142.1; PID:q2983570; GB:AE00065

A:Experimental source: strain VF5
C:Genetics:
A:Gene: mtfa

Query Match 72.9%; Score 35; DB 2; Length 588;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
| : |||||
Db 432 KAFEILWKK 440

RESULT 5
T43447
hypothetical protein DKFZp434J1217.1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Sep-2000
C:Accession: T43447
R:Blocker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z22513
A:Accession: T43447
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-795 <AAA>
A:Cross-references: EMBL:AL133608
A:Experimental source: adult testis; clone DKF2p434J1217
C:Genetics:
A:Note: DKFZp434J1217.1
C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match 72.9%; Score 35; DB 2; Length 795;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWK 8
: |||||
Db 594 QQLQILWK 601

RESULT 6
JH0225
L96 protein - Tipula iridescent virus
C:Species: Tipula iridescent virus
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: JH0225
R:Home, W.A.; Tajbakhsh, S.; Seligy, V.L.
Gene 94, 243-248, 1990
A:Title: Molecular cloning and characterization of a late Tipula iridescent virus gen
A:Reference number: JH0225; MUID:91078646; PMID:1701750
A:Accession: JH0225
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-867 <HOM>
A:Cross-references: GB:M34853; NID:g335215; PIDN:AAA47919.1; PID:g335216

Query Match 72.9%; Score 35; DB 2; Length 867;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
||| | |||
Db 152 KKLDIDWKK 160

RESULT 7
T00133
RNA-directed RNA polymerase (EC 2.7.7.48) - rice grassy stunt virus
C:Species: rice grassy stunt virus
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000
C:Accession: T00133
R:Toriyama, S.; Kimishima, T.; Takahashi, M.; Shimizu, T.; Minaka, N.; Akutsu, K.

J. Gen. Virol. 79, 2051-2058, 1998
A:Title: The complete nucleotide sequence of the rice grassy stunt virus genome and gene
A:Reference number: Z14118; MUID:98378059; PMID:9714257
A:Accession: T00133
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: genomic RNA
A:Residues: 1-2925 <TOR>
A:Cross-references: EMBL:AH009656; NID:g3410897; PIDN:AAA32246.1; PID:g3410899
A:Experimental source: isolate IRRI
C:Keywords: nucleotidyltransferase

Query Match 72.9%; Score 35; DB 2; Length 2925;
Best Local Similarity 66.7%; Pred. No. 4.5e-02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
| | | | |
DB 2209 KTLXIVWKK 2217

RESULT 8
D86439
Protein T19E23.15 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C:Accession: D86439
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86439
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-137 <STO>
A:Cross-references: GB:AE005172; NID:g6692124; PIDN:AAF24589.1; GSPDB:GN00141
C:Genetics:
A:Gene: T19E23.15
A:Map position: 1
C:Superfamily: rat ribosomal protein L21

Query Match 70.8%; Score 34; DB 2; Length 137;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LQILWKK 9
| | | | |
DB 5 LEVLWKK 11

RESULT 9
W6WLB5
E6 protein - human papillomavirus type 5b
C:Species: human papillomavirus type 5b
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jun-2000
C:Accession: E40480
R:Yabe, Y.; Sakai, A.; Hitsumoto, T.; Kato, H.; Ogura, H.
Virology 183, 793-798, 1991
A:Title: A subtype of human papillomavirus 5 (HPV-5b) and its subgenomic segment amplifi
A:Reference number: A40480; MUID:91306467; PMID:1649510
A:Accession: E40480
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-157 <YAB>
A:Cross-references: GB:D90252; NID:g222395; PIDN:BAA14292.1; PID:g222398
C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger
F:41-77/Region: zinc finger CCCC motif
F:114-150/Region: zinc finger CCCC motif

Query Match 70.8%; Score 34; DB 1; Length 157;
Best Local Similarity 62.5%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLQILWKK 8
| | | | |
DB 59 KKLSLWKK 66

RESULT 10
B72277

phosphoribosylglycinamide formyltransferase - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: B72277
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; H
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: B72277
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-205 <ARN>
A:Cross-references: GB:AE001780; GB:AE000512; NID:g4981796; PIDN:AAD36323.1; PID:g49
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1248
C:Superfamily: phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamid

Query Match 70.8%; Score 34; DB 2; Length 205;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
| | | | |
DB 56 KKLQIPWER 64

RESULT 11

B86397
Protein T7N9.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: B86397
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzi
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B86397
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-308 <STO>
A:Cross-references: GB:AE005172; NID:g8778853; PIDN:AAF79852.1; GSPDB:GN00141
C:Genetics:
A:Gene: T7N9.8
A:Map position: 1

Query Match 70.8%; Score 34; DB 2; Length 308;
Best Local Similarity 71.4%; Pred. No. 74;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILW 7
Db 93 KKVQVLW 99
RESULT 12
B64216
hemolysin tlyC homolog - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999
C:Accession: B64216
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: B64216
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-424 <TIGR>
A:Cross-references: GB:U39694; GR:L43967; NID:g1045822; PID:g1045829; TIGR:MG146
A:Experimental source: strain G-37
C:Genetics:
C:Superfamily: hemolysin homolog tlyC

Query Match 70.8%; Score 34; DB 1; Length 424;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
Db 207 KKVMIKWK 215
RESULT 13
T19491
hypothetical protein C26E1.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T19491
R:Sims, M.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19130
A:Accession: T19491
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-451 <WIL>
A:Cross-references: EMBL:Z81040; PIDN:CA802783.i; GSPDR:GN00023; CESP:C26E1.3
A:Experimental source: clone C26E1
C:Genetics:
A:Gene: CESP:C26E1.3
A:Map position: 5
A:Introns: 16/3; 51/2; 164/3; 198/3; 249/3; 303/2; 348/3; 385/3; 408/2
C:Superfamily: Caenorhabditis elegans hypothetical protein C26E1.3

Query Match 70.8%; Score 34; DB 2; Length 451;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWKK 8
Db 353 KKLFLWQ 360

RESULT 14
JC4239
phospholipase A2-activating protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 26-May-2000
C:Accession: JC4239

R:Wang, H.; Lemasters, J.J.; Herman, B.
Gene 161, 237-241, 1995
A:Title: Cloning of a rat cDNA encoding a protein with high homology to mouse phospho
A:Reference number: JC4239; MUID:95394363; PMID:7665086
A:Accession: JC4239
A:Molecule type: mRNA
A:Residues: 1-647 <WAN>
A:Cross-references: GB:U17901
A:Experimental source: hepatocytes
A:Note: This protein has a homologous region, 503-538, with bee venom melittin
C:Comment: This protein is rich in cysteine, it contains fifteen Cys residues in the
C:Genetics:
A:Gene: hcv9
C:Superfamily: unassigned WD repeat proteins; WD repeat homology
F:90-123/Domain: WD repeat homology <WD1>
F:130-162/Domain: WD repeat homology <WD2>
F:170-203/Domain: WD repeat homology <WD3>

Query Match 70.8%; Score 34; DB 2; Length 647;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWKK 8
Db 537 QQLQVLWKK 544

RESULT 15
S76045
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S76045
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
S.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76045
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1042 <KAN>
A:Cross-references: EMBL:D63999; GB:AB001339; NID:g1001396; PIDN:BAAL0023.1; PID:g10C
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: Saccharomyces alpha-mannosidase

Query Match 70.8%; Score 34; DB 2; Length 1042;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
Db 545 EKLELWKK 553

Search completed: October 14, 2003, 14:38:06
Job time : 14.8125 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 ; Search time 6.375 Seconds
(without alignments)
66.391 Million cell updates/sec

Title: US-09-881-490-163
Perfect score: 48
Sequence: 1 KKLQILWKK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 39 | 81.2 | 339 | 1 RT13_YEAST | P12686 saccharomyc |
| 2 | 39 | 81.2 | 1273 | 1 YAR2_SCHPO | Q10135 schizosacch |
| 3 | 36 | 75.0 | 168 | 1 VE6_HPV21 | P28832 human papil |
| 4 | 35 | 72.9 | 279 | 1 LACR_STAXY | Q33813 staphylococ |
| 5 | 35 | 72.9 | 546 | 1 PLAP_MOUSE | P27612 mus musculu |
| 6 | 35 | 72.9 | 738 | 1 PLAP_HUMAN | Q9Y263 homo sapien |
| 7 | 35 | 72.9 | 740 | 1 NLD2_HUMAN | Q9Y390 homo sapien |
| 8 | 35 | 72.9 | 867 | 1 VL96_IRV1 | P22856 tipula irid |
| 9 | 34 | 70.8 | 157 | 1 VE6_HPV36 | P50810 human papil |
| 10 | 34 | 70.8 | 157 | 1 VE6_HPV5B | P26556 human papil |
| 11 | 34 | 70.8 | 171 | 1 VE6_HPV14 | P28830 human papil |
| 12 | 34 | 70.8 | 424 | 1 Y146_MYCGE | Q43399 mycoplasma |
| 13 | 34 | 70.8 | 647 | 1 PLAP_RAT | P54319 rattus norv |
| 14 | 33 | 68.8 | 142 | 1 VE6_HPV32 | P36810 human papil |
| 15 | 33 | 68.8 | 156 | 1 VE6_HPV47 | P22422 human papil |
| 16 | 33 | 68.8 | 165 | 1 VE6_HPV20 | P28831 human papil |
| 17 | 33 | 68.8 | 493 | 1 OCLN_XENLA | Q9pun1 xenopus lae |
| 18 | 33 | 68.8 | 502 | 1 RK11_SECC | Q02723 secale cere |
| 19 | 33 | 68.8 | 514 | 1 CP24_HUMAN | Q07973 homo sapien |
| 20 | 33 | 68.8 | 578 | 1 TREA_RABIT | P19813 oryctolagus |
| 21 | 32 | 66.7 | 159 | 1 VE6_HPV27 | P36808 human papil |
| 22 | 32 | 66.7 | 161 | 1 VE6_HPV25 | P28833 human papil |
| 23 | 32 | 66.7 | 178 | 1 ARF3_CAEEL | Q94231 caenorhabdi |
| 24 | 32 | 66.7 | 338 | 1 PHND_ECOLI | P16682 escherichia |
| 25 | 32 | 66.7 | 452 | 1 RN18_HUMAN | Q9ns80 homo sapien |
| 26 | 32 | 66.7 | 489 | 1 NIFD_ALCFA | Q44045 alcaligenes |
| 27 | 32 | 66.7 | 518 | 1 DRT2_ARATH | Q05763 arabidopsis |
| 28 | 32 | 66.7 | 535 | 1 DCTS_RACSU | P96601 bacillus su |
| 29 | 32 | 66.7 | 645 | 1 REP_BUCAI | P57654 buchnera ap |
| 30 | 31 | 64.6 | 157 | 1 VE6_HPV05 | P06930 human papil |
| 31 | 31 | 64.6 | 166 | 1 VE6_HPV19 | P36806 human papil |
| 32 | 31 | 64.6 | 185 | 1 SSRG_HUMAN | Q9un12 homo sapien |
| 33 | 31 | 64.6 | 185 | 1 SSRG_RAT | Q08013 rattus norv |

| | | | | | |
|----|----|------|-----|--------------|--------------------|
| 34 | 31 | 64.6 | 195 | 1 ENGB_THEMA | Q9xlh7 thermotoga |
| 35 | 31 | 64.6 | 196 | 1 GIDB_AQUAE | O67522 aquifex aeo |
| 36 | 31 | 64.6 | 214 | 1 STL4_SOLTU | Q41495 solanum tub |
| 37 | 31 | 64.6 | 263 | 1 MT04_MYCTU | P66390 mycobacteri |
| 38 | 31 | 64.6 | 283 | 1 YF46_ARCFU | O28726 archaeoglob |
| 39 | 31 | 64.6 | 350 | 1 PE24_ARATH | Q9zv04 arabidopsis |
| 40 | 31 | 64.6 | 416 | 1 SO_DROME | O27350 drosophila |
| 41 | 31 | 64.6 | 483 | 1 YC24_GUITH | O78473 guillardia |
| 42 | 31 | 64.6 | 489 | 1 COAT_FMVD | P09519 figwort mos |
| 43 | 31 | 64.6 | 519 | 1 TRPE_BUCDN | Q44697 buchnera ap |
| 44 | 31 | 64.6 | 540 | 1 BS61_RABIT | Q05004 oryctolagus |
| 45 | 31 | 64.6 | 580 | 1 P69_MYCHR | P15362 mycoplasma |

ALIGNMENTS

RESULT 1
RT13_YEAST
ID RT13_YEAST STANDARD; PRT; 339 AA.
AC P12686;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 40S ribosomal protein S13, mitochondrial precursor.
GN MRP13 OR YGR084C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE OF 28-339 FROM N.A.
RX MEDLINE=89127203; PubMed=3065621;
RA Partaledis J.A., Mason T.L.;
RT "Structure and regulation of a nuclear gene in Saccharomyces
RT cerevisiae that specifies MRP13, a protein of the small subunit of
RT the mitochondrial ribosome."
RL Mol. Cell. Biol. 8:3647-3660(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA Wedler H., Scharfe M., Wedler E., Wambutt R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: COMPONENT OF THE SMALL SUBUNIT OF MITOCHONDRIAL
CC RIBOSOME.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; 272869; CAA97086.1; -;
DR EMBL; M22109; AAA34788.1; -;
DR PIR; S64379; R6BY13.
DR SGD; S0003316; MRP13.
KW Ribosomal protein; Mitochondrion; Transit peptide.
FT TRANSIT 1 37 MITOCHONDRION (POTENTIAL).
FT CHAIN 38 339 40S RIBOSOMAL PROTEIN S13.
FT CONFLICT 114 114 T -> S (IN REF. 1).
FT CONFLICT 310 339 ESSDPYDTHLKALGLLETPPPQESTEKEEK -> RIQRSIR
FT HAPESVGTGNTLSGSGRGRKIVQNTHRKYINNIL (IN
FT REF. 1).
SQ SEQUENCE 339 AA; 38988 MW; 89DC5A71799F2CEE CRC64;

Query Match 81.2%; Score 39; DB 1; Length 339;
Best Local Similarity 66.7%; Pred. No. 3.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KKLQILWKK 9
:|||: |||

```
Db 209 RKLOVAVKK 217

RESULT 2
YAR2_SCHPO
ID YAR2_SCHPO STANDARD; PRT; 1273 AA.
AC Q10135;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein C23E2.02 in chromosome I.
GN SPAC23E2.02.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeil C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Roy F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- SIMILARITY: Contains 1 HMG box domain.
CC -----
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CC -----
DR EMBL: Z68887; CAA93114.1; -.
DR PIR: T38292; T38292.
DR GeneDB_SPombe; SPAC23E2.02; -.
DR InterPro; IPR002937; Amino_oxidase.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF01593; Amino_oxidase; 1.
DR Pfam; PF04433; SWIRM; 1.
DR PROSITE; PS0118; HMG_BOX_2; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 1028 1048 POTENTIAL.
FT DNA_BIND 1115 1195 HMG_BOX.
SQ SEQUENCE 1273 AA; 142489 MW; 3FEFF6433DF3C0B6 CRC64;

Query Match 81.2%; Score 39; DB 1; Length 1273;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 209 RKLOVAVKK 217

RESULT 3
VE6_HP21
ID VE6_HP21 STANDARD; PRT; 168 AA.
AC P28832;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 21.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=31548;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92124737; PubMed=1310189;
RA Kiyono T., Hiraiwa A., Ishibashi M.;
RT "Differences in transforming activity and coded amino acid sequence
RT among E6 genes of several papillomaviruses associated with
RT epidermodysplasia verruciformis.";
RL Virology 186:628-639(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----
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CC -----
DR EMBL: D90263; BAA14310.1; -.
DR EMBL: U31779; AAA79394.1; -.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW Early protein; DNA-binding; Nuclear protein; Zinc-finger.
FT ZN_FING 55 91 POTENTIAL.
FT ZN_FING 128 164 POTENTIAL.
FT CONFLICT 130 130 T -> N (IN REF. 2).
FT CONFLICT 148 148 H -> F (IN REF. 2).
FT CONFLICT 156 156 T -> S (IN REF. 2).
SQ SEQUENCE 168 AA; 19290 MW; 744E8AF8FOACE53C CRC64;

Query Match 75.0%; Score 36; DB 1; Length 168;
Best Local Similarity 75.0%; Pred. No. 6.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 73 KKLQILWK 80

RESULT 4
LACR_STAXY
ID LACR_STAXY STANDARD; PRT; 279 AA.
AC O33813;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Lactose operon transcription activator.
GN LACR.
```

```
OS Staphylococcus xylosum.
OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
OX NCBI_TaxID=1288;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 20267 / Isolate C2A;
RX MEDLINE=98233718; PubMed=9573174;
RA Bassias J., Brueckner R.;
RT "Regulation of lactose utilization genes in Staphylococcus xylosum."
RL J. Bacteriol. 180:2273-2279(1998).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR OF THE LACPH GENES FOR
CC LACTOSE UTILIZATION.
CC -1- SIMILARITY: BELONGS TO THE ARAC/YXLS FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC -----
CC EMBL: Y14599; CAA74935.1;
DR InterPro: IPR000005; HTHARAC.
DR Pfam: PF00165; HTH_ARAC; 2.
DR SMART: SM00342; HTH_ARAC; 1.
DR PROSITE: PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE: PS01124; HTH_ARAC_FAMILY_2; 1.
KW Transcription regulation; DNA-binding; Activator.
FT DNA_BIND 190 209 H-T-H motif (BY SIMILARITY).
SQ SEQUENCE 279 AA; 32335 MW; 304CDF65A7H14D34 CRC64;

Query Match 72.9%; Score 35; DB 1; Length 279;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 IQILWKK 9
Db 1 MQVLWKK 7
:|:|:|:|

RESULT 5
PLAP_MOUSE STANDARD; PRT; 646 AA.
ID PLAP_MOUSE
AC P27612;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A-2-activating protein (PLAP).
GN PLAA OR PLAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91271400; PubMed=2052621;
RA Clark M.A., Oezguer L.E., Conway T.M., Disposito J., Crooke S.T.,
RA Bomalaski J.S.;
RT "Cloning of a phospholipase A2-activating protein."
RL Proc. Natl. Acad. Sci. U.S.A. 88:5418-5422(1991).
RN [2]
RP REVISIONS.
RX MEDLINE=95394363; PubMed=7665086;
RA Wang H., Lenasters J.J., Herman B.;
RT "Cloning of a rat cDNA encoding a protein with high homology to mouse
RT phospholipase A2-activating protein."
RL Gene 161:237-241(1995).
CC -1- FUNCTION: PLAY AN IMPORTANT ROLE IN THE REGULATION OF SPECIFIC
CC INFLAMMATORY DISEASE PROCESSES.
CC -1- INDUCTION: IN SMOOTH MUSCLE & ENDOTHELIAL CELLS BY LEUKOTRIENE D4,
CC BY TUMOR NECROSIS FACTOR IN ENDOTHELIAL CELLS AND BY URIC ACID
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CC CRYSTALS IN MACROPHAGES.
CC -1- SIMILARITY: Contains 6 WD repeats.
CC -1- SIMILARITY: BELONGS TO THE PLAP FAMILY OF WD-REPEAT PROTEINS.
CC -----
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CC -----
CC EMBL: M57958; AAA39943.1; ALT_SEQ.
DR MGD; MGI:104810; Plaa.
DR GO: GO:0016005; F:phospholipase A2 activator activity; IDA.
DR GO: GO:0005515; F:protein binding activity; IPI.
DR GO: GO:0006954; P:inflammatory response; IDA.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 6.
DR PRINTS: PR00320; GPROTEINBRPT.
DR ProDom: PD000018; WD40; 1.
DR SMART: SM00320; WD40; 5.
DR PROSITE: PS00678; WD_REPEATS_1; FALSE_NEG.
DR PROSITE: PS50082; WD_REPEATS_2; 3.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT REPEAT 6 41 WD 1.
FT REPEAT 53 82 WD 2.
FT REPEAT 92 122 WD 3.
FT REPEAT 132 161 WD 4.
FT REPEAT 172 202 WD 5.
FT REPEAT 212 241 WD 6.
SQ SEQUENCE 646 AA; 71416 MW; 8219C118DBE080C5 CRC64;

Query Match 72.9%; Score 35; DB 1; Length 646;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWK 8
Db 537 QQLQILWK 544
:|:|:|:|:|

RESULT 6
PLAP_HUMAN STANDARD; PRT; 738 AA.
ID PLAP_HUMAN
AC Q9Y263; Q9Y5L1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A-2-activating protein (PLAP) (PLA2P).
GN PLAA OR PLAP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RA Ruiz A., Nadal M., Puig S., Estivill X.;
RT "Cloning of the human phospholipase A2 activating protein (hPLAP) gene
RT on the chromosome 9p21 melanoma deleted region."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99132024; PubMed=9931468;
RA Chopra A.K., Ribardo D.A., Wood T.G., Prusak D.J., Xu X.-J.,
RA Peterson J.W.;
RT "Molecular characterization of cDNA for phospholipase A2-activating
RT protein."
RL Biochim. Biophys. Acta 1444:125-130(1999).
RN [3]
RP SEQUENCE FROM N.A.
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RX MEDLINE-20112769; PubMed-10644453;
RA Beatty B., Qi S., Pienkowska M., Scherer S.W., Testa J.R., Cheng J.Q.,
RA Herbrick J.A., Scheidl T., Zhang Z., Koia I., Seth A.;
RT "Chromosomal localization of phospholipase A2 activating protein, an
RT ets2 target gene, to 9p21.";
RL Genomics 62:529-532(1999).
CC -!- FUNCTION: PLAY AN IMPORTANT ROLE IN THE REGULATION OF SPECIFIC
CC INFLAMMATORY DISEASE PROCESSES (BY SIMILARITY).
CC -!- SIMILARITY: Contains 6 WD repeats.
CC -!- SIMILARITY: BELONGS TO THE PLAP FAMILY OF WD-REPEAT PROTEINS.
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITION 642
CC ONWARD DUE TO A FRAMESHIFT.
CC -----
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CC -----
DR EMBL; AJ238243; CAR42881.1; -.
DR EMBL; AF083395; AAD03030.1; -.
DR EMBL; AF145020; AAD42075.1; ALT_FRAME.
DR Genew; HGNC:9043; PLAA.
DR MIM; 603873; -.
DR GO; GO:0016005; F:phospholipase A2 activator activity; TAS.
DR GO; GO:0006644; P:phospholipid metabolism; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR001580; WD40.
DR Pfam; PF00400; WD40; 6.
DR PRINTS; PR00320; GPROTEINBRPT.
DR PRODOM; PD000018; WD40; 1.
DR SMART; SM00320; WD40; 6.
DR PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
DR PROSITE; PS50082; WD_REPEATS_2; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT REPEAT 6 50 WD 1.
FT REPEAT 53 91 WD 2.
FT REPEAT 92 131 WD 3.
FT REPEAT 133 170 WD 4.
FT REPEAT 172 211 WD 5.
FT REPEAT 213 250 WD 6.
FT CONFLICT 29 29 A -> F (IN REF. 3).
FT CONFLICT 40 40 F -> L (IN REF. 3).
FT CONFLICT 365 365 I -> A (IN REF. 3).
FT CONFLICT 474 474 M -> L (IN REF. 3).
FT CONFLICT 484 484 V -> L (IN REF. 3).
SQ SEQUENCE 738 AA; 80826 MW; F2DB210E5C9B381A CRC64;

Query Match 72.9%; Score 35; DB 1; Length 738;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWK 8
DB 537 QQLQILWK 544

RESULT 7
NLD2_HUMAN STANDARD; PRT; 740 AA.
AC Q9Y3Q0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE N-acetylated-alpha-linked acidic dipeptidase II (EC 3.4.17.21)
DE (NAALADase II).
GN NAALAD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung carcinoma;
RX MEDLINE-99185063; PubMed-10085079;
RA Pangalos M.N., Neefs J.-M., Somers M., Verhasselt P., Bekkers M.,
RA van der Helm L., Fraiponts E., Ashton D., Gordon R.D.;
RT "Isolation and expression of novel human glutamate carboxypeptidases
RT with N-acetylated alpha-linked acidic dipeptidase and dipeptidyl
RT peptidase IV activity.";
RL J. Biol. Chem. 274:8470-8483(1999).
CC -!- FUNCTION: Has N-acetylated-alpha-linked-acidic dipeptidase IV type
CC (NAALADase) activity. Also exhibits a dipeptidyl-peptidase IV type
CC activity. In vitro, cleaves Gly-Pro-AMC.
CC -!- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal
CC glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.
CC -!- COFACTOR: zinc; Binds two ions per subunit. Required for NAALADase
CC activity.
CC -!- ENZYME REGULATION: Inhibited by quisqualate.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Highest expression in the testis. Also found
CC in ovary and spleen. Weak expression in prostate, heart and
CC placenta. In brain, expressed in striatum, parietal cortex and
CC ventral striatum with lower levels in hippocampus, brain stem,
CC putamen and superior colliculus.
CC -!- DOMAIN: The NAALADase activity is found in the central region, the
CC dipeptidyl peptidase IV type activity in the C-terminal.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
CC -----
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CC -----
DR EMBL; AJ012370; CAB39967.1; -.
DR MEROPS; M28.012; -.
DR Genew; HGNC:14526; NAALAD2.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0004180; F:carboxypeptidase activity; NAS.
DR GO; GO:0016805; F:dipeptidase activity; NAS.
DR GO; GO:0004274; F:dipeptidyl-peptidase IV activity; NAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR003137; PA.
DR Pfam; PF02225; PA; 1.
DR Pfam; PF04389; Peptidase_M28; 1.
DR Pfam; PF04253; TFR_dimer; 1.
DR Hydrolase; Carboxypeptidase; Metalloprotease; Zinc; Aminopeptidase;
KW Dipeptidase; Serine protease; Transmembrane; Glycoprotein;
KW Signal-anchor; Multifunctional enzyme.
FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 8 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 32 740 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 264 577 NAALADASE.
FT ACT_SITE 414 414 NUCLEOPHILE (NAALADASE) (BY SIMILARITY).
FT ACT_SITE 618 618 CHARGE RELAY SYSTEM (POTENTIAL).
FT ACT_SITE 656 656 CHARGE RELAY SYSTEM (POTENTIAL).
FT ACT_SITE 679 679 CHARGE RELAY SYSTEM (POTENTIAL).
FT METAL 367 367 ZINC 2 (BY SIMILARITY).
FT METAL 377 377 ZINC 1 AND 2 (BY SIMILARITY).
FT METAL 415 415 ZINC 1 (BY SIMILARITY).
FT METAL 443 443 ZINC 2 (BY SIMILARITY).
FT METAL 543 543 ZINC 1 (BY SIMILARITY).
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 449 449 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
```



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SQ SEQUENCE 740 AA; 83591 MW; 040624D691ECF879 CRC64;
Query Match 72.9%; Score 35; DB 1; Length 740;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
   ||:| |||
Db 84 KKIQTQWKK 92

RESULT 8
VL96_IRV1
ID VL96_IRV1 STANDARD; PRT; 867 AA.
AC P22856;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE L96 protein.
GN L96.
OS Tipula iridescent virus (TIV) (Insect iridescent virus type 1).
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
OX NCBI_TaxID=10490;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91078646; PubMed=1701750;
RA Home W.A., Tajbakhsh S., Seligy V.L.;
RT "Molecular cloning and characterization of a late Tipula iridescent
   virus gene.";
RT virus gene.";
RL Gene 94:243-248(1990).
CC -1- FUNCTION: MAY BE INVOLVED IN TIV GENOMIC DNA PACKAGING IN A
   MANNER RELATED TO THE GAG POLYPROTEINS OF THE MAMMALIAN VIRUSES.
CC -1- SIMILARITY: Contains 1 OTU domain.
CC -----
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CC -----
CC EMBL; M62953; AAA47919.1; -.
CC PIR; JH0225; JH0225.
CC InterPro; IPR003323; OTU.
CC Pfam; PF02338; OTU; 1.
CC PROSITE; PS50802; OTU; 1.
CC Repeat; DNA packaging; DNA-binding.
CC DOMAIN 606 745 OTU.
CC SEQUENCE 867 AA; 96011 MW; F19DBDE8FE5CA103 CRC64;

Query Match 72.9%; Score 35; DB 1; Length 867;
Best Local Similarity 77.8%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
   ||| : |||
Db 152 KKLIDIDWKK 160

RESULT 9
VE6_HPV36
ID VE6_HPV36 STANDARD; PRT; 157 AA.
AC P50810;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 36.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=37957;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----
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CC -----
CC EMBL; U31785; AAA79436.1; -.
CC InterPro; IPR001334; E6.
CC Pfam; PF00518; E6; 1.
CC Early protein; DNA-binding; Nuclear protein; Zinc-finger.
FT 2N_FING 41 77 POTENTIAL.
FT 2N_FING 114 150 POTENTIAL.
SQ SEQUENCE 157 AA; 18123 MW; ECB6CE02C0ECB126 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 157;
Best Local Similarity 62.5%; Pred. No. 14;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLQILWKK 8
   ||| : |||
Db 59 KKLSLIWK 66

RESULT 10
VE6_HPV5B
ID VE6_HPV5B STANDARD; PRT; 157 AA.
AC P26556;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 5b.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10599;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91306467; PubMed=1649510;
RA Yabe Y., Sakai A., Hitsumoto T., Kato H., Ogura H.;
RT "A subtype of human papillomavirus 5 (HPV-5b) and its subgenomic
   segment amplified in a carcinoma: nucleotide sequences and genomic
   organizations.";
RT Virology 183:793-798(1991).
RL -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----
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CC -----
CC EMBL; D90252; BAA14292.1; -.
CC PIR; E40480; W6WLB5.
CC InterPro; IPR001334; E6.
CC Pfam; PF00518; E6; 1.
CC Early protein; DNA-binding; Nuclear protein; Zinc-finger.
FT 2N_FING 41 77 POTENTIAL.
FT 2N_FING 114 150 POTENTIAL.
```



```
SQ SEQUENCE 157 AA; 18087 MW; 20684H7EF730AA47 CRC64;
Query Match 70.8%; Score 34; DB 1; Length 157;
Best Local Similarity 62.5%; Pred. No. 14;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKQLQILWK 8
   ||| :||
DB 59 KKLSLIWK 66

RESULT 11
VE6_HP14
ID VE6_HP14 STANDARD; PRT; 171 AA.
AC P28830;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 14.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10605;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92124737; PubMed=1310189;
RA Kiyono T., Hiraiwa A., Ishibashi M.;
RT "Differences in transforming activity and coded amino acid sequence
RT among E6 genes of several papillomaviruses associated with
RT epidermodysplasia verruciformis.";
RL Virology 186:628-639(1992).
CC -!- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----
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CC -----
DR EMBL; D90262; BAA14309.1; -
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW Early protein; DNA-binding; Nuclear protein; Zinc-finger.
FT ZN_FING 58 94 POTENTIAL.
FT ZN_FING 131 157 POTENTIAL.
SQ SEQUENCE 171 AA; 19214 MW; 394FBD3E5903F69F CRC64;

Query Match 70.8%; Score 34; DB 1; Length 171;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKQLQILWK 8
   ||| :||
DB 76 KKLSLIWK 83

RESULT 12
Y146_MYCGE
ID Y146_MYCGE STANDARD; PRT; 424 AA.
AC Q49399;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MGL46 (VXpSP7_orf424).
GN MGL46 OR MPN159 OR MP672.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bitt K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE UPF0053 FAMILY.
CC -!- SIMILARITY: Contains 2 CBS domains.
CC -----
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CC -----
DR EMBL; U39695; AAC71364.1; -
DR PIR; B64216; B64216.
DR TIGR; MG146; -.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR002550; DUF21.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF01595; DUF21; 1.
DR SMART; SM00116; CBS; 2.
KW Hypothetical protein; CBS domain; Repeat; Transmembrane;
KW Complete proteome.
FT TRANSMEM 7 27 POTENTIAL.
FT TRANSMEM 71 91 POTENTIAL.
FT TRANSMEM 101 121 POTENTIAL.
FT TRANSMEM 135 155 POTENTIAL.
SQ SEQUENCE 424 AA; 48720 MW; A361AAE5B995DA87 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 424;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKQLQILWK 9
   ||| :|||
DB 207 KKVMIKWK 215

RESULT 13
PLAP_RAT
ID PLAP_RAT STANDARD; PRT; 647 AA.
AC P54319;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A-2-activating protein (PLAP).
GN PLAA OR PLAP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=95394363; PubMed=7665086;
RA Wang H., Lemasters J.J., Herman B.;
RT "Cloning of a rat cDNA encoding a protein with high homology to mouse
RT phospholipase A2-activating protein.";
RL Gene 161:237-241(1995).
CC -!- FUNCTION: PLAY AN IMPORTANT ROLE IN THE REGULATION OF SPECIFIC
CC INFLAMMATORY DISEASE PROCESSES.
CC -!- SIMILARITY: Contains 6 WD repeats.
```

```
CC -1st SIMILARITY: BELONGS TO THE PLAP FAMILY OF WD-REPEAT PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch.)
CC -----
CC EMBL: U17901; AAA79979.1; ALT_SEQ.
CC PIR: JC4239; JC4239.
CC InterPro: IPR001680; WD40.
CC Pfam: PF00400; WD40; 6.
CC PRINTS: PR00320; GPROTEINBRPT.
CC PRODOM: PD000018; WD40; 1.
CC SMART: SM00320; WD40; 6.
CC PROSITE: PS00678; WD_REPEATS_1; FALSE_NEG.
CC PROSITE: PS50082; WD_REPEATS_2; 3.
CC PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT REPEAT 6 41 WD 1.
FT REPEAT 53 82 WD 2.
FT REPEAT 92 122 WD 3.
FT REPEAT 132 161 WD 4.
FT REPEAT 172 202 WD 5.
FT REPEAT 212 241 WD 6.
SQ SEQUENCE 647 AA; 71187 MW; B0A8BD230AC5300C CRC64;

Query Match 70.8%; Score 34; DB 1; Length 647;
Best Local Similarity 62.5%; Pred. NO. 60;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWK 8
Db 537 QQLQVLWK 544

RESULT 14
VE6_HPV32 STANDARD; PRT; 142 AA.
AC P36810;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 32.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10612;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----
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CC -----
CC EMBL: X74475; CAA52549.1; -.
CC PIR: S36509; S36509.
CC InterPro: IPR001334; E6.
CC Pfam: PF00518; E6; 1.
```

```
DR SMART; SM00355; ZnF_C2H2; 1.
KW Early protein; DNA-binding; Nuclear protein; Zinc-finger.
FT ZN_FING 31 67 POTENTIAL.
FT ZN_FING 104 140 POTENTIAL.
SQ SEQUENCE 142 AA; 16631 MW; 7E108DDE4A72F297 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 142;
Best Local Similarity 55.6%; Pred. NO. 20;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKLQILWK 9
Db 49 KDLHVWVK 57

RFSULT 15
VE6_HPV47 STANDARD; PRT; 156 AA.
AC P22422;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 47.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10594;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90281611; PubMed=2162112;
RA Kiyono T., Adachi A., Ishibashi M.;
RT "Genome organization and taxonomic position of human papillomavirus
RT type 47 inferred from its DNA sequence.";
RL Virology 177:401-405(1990).
CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----
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CC -----
CC EMBL: M32305; AAA46976.1; -.
CC PIR: A35324; W6WL47.
CC InterPro: IPR001334; E6.
CC Pfam: PF00518; E6; 1.
KW Early protein; DNA-binding; Nuclear protein; Zinc-finger.
FT ZN_FING 40 76 POTENTIAL.
FT ZN_FING 113 149 POTENTIAL.
SQ SEQUENCE 156 AA; 18116 MW; A2AF8D1B95BCE623 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 156;
Best Local Similarity 62.5%; Pred. NO. 22;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLQILWK 8
Db 58 KKLILWK 65
```

Search completed: October 14, 2003, 14:34:08
Job time : 8.54167 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 ; Search time 29.8125 Seconds
(without alignments)
77.903 Million cell updates/sec

Title: US-09-881-490-163
Perfect score: 48
Sequence: 1 KKLQILWKK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTRMBL_23:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriaph:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 40 | 83.3 | 366 | 8 Q8HUW9 | Q8huw9 ulmus ameri |
| 2 | 39 | 81.2 | 701 | 11 Q8BQ23 | Q8bq23 mus musculu |
| 3 | 39 | 81.2 | 731 | 11 Q9JIE5 | Q9jie5 mus musculu |
| 4 | 39 | 81.2 | 745 | 11 Q9JI20 | Q9ji20 mus musculu |
| 5 | 39 | 81.2 | 745 | 11 Q8CC51 | Q8cc51 mus musculu |
| 6 | 39 | 81.2 | 746 | 11 P97616 | P97616 rattus norv |
| 7 | 38 | 79.2 | 446 | 4 Q96BQ3 | Q96bq3 homo sapien |
| 8 | 38 | 79.2 | 564 | 10 Q9LSS5 | Q9lss5 arabidopsis |
| 9 | 38 | 79.2 | 739 | 4 Q9NS39 | Q9ns39 homo sapien |
| 10 | 38 | 79.2 | 900 | 5 Q8I634 | Q8i634 plasmodium |
| 11 | 37 | 77.1 | 148 | 12 Q8JNA1 | Q8jna1 human papil |
| 12 | 36 | 75.0 | 208 | 4 Q9BOW4 | Q9bow4 homo sapien |
| 13 | 36 | 75.0 | 279 | 16 Q8XMB9 | Q8xmb9 cistridium |
| 14 | 36 | 75.0 | 375 | 4 Q8IW24 | Q8iw24 homo sapien |
| 15 | 36 | 75.0 | 716 | 11 Q8K5B1 | Q8k5b1 mus musculu |
| 16 | 36 | 75.0 | 716 | 11 Q8R501 | Q8r501 mus musculu |

| | | | | | |
|----|----|------|------|-----------|--------------------|
| 17 | 36 | 75.0 | 822 | 5 Q9BMX6 | Q9bmX6 aplysia cal |
| 18 | 36 | 75.0 | 1102 | 5 Q8IRF5 | Q8irf5 drosophila |
| 19 | 36 | 75.0 | 2217 | 13 Q8AV57 | Q8av57 gallus gall |
| 20 | 35 | 72.9 | 293 | 10 Q9FWJ9 | Q9fwj9 arabidopsis |
| 21 | 35 | 72.9 | 317 | 4 Q8IUX3 | Q8iux3 homo sapien |
| 22 | 35 | 72.9 | 326 | 5 Q45738 | Q45738 caenorhabdi |
| 23 | 35 | 72.9 | 357 | 8 Q8HUX0 | Q8hux0 ampelocera |
| 24 | 35 | 72.9 | 588 | 16 Q67183 | Q67183 aquifex aeo |
| 25 | 35 | 72.9 | 718 | 10 Q82779 | Q82779 adiantum ca |
| 26 | 35 | 72.9 | 794 | 11 Q8C6C4 | Q8c6c4 mus musculu |
| 27 | 35 | 72.9 | 795 | 4 Q9NVE9 | Q9nve9 homo sapien |
| 28 | 35 | 72.9 | 795 | 4 Q9UF53 | Q9uf53 homo sapien |
| 29 | 35 | 72.9 | 895 | 11 Q8C117 | Q8c117 mus musculu |
| 30 | 35 | 72.9 | 1043 | 16 Q9CMV5 | Q9cmv5 pasteurella |
| 31 | 35 | 72.9 | 2241 | 12 Q91HJ2 | Q91hj2 avian param |
| 32 | 35 | 72.9 | 2925 | 12 Q89163 | Q89163 rice grassy |
| 33 | 35 | 72.9 | 2925 | 12 Q9JGN8 | Q9jgn8 rice grassy |
| 34 | 34 | 70.8 | 62 | 12 Q91GK8 | Q91gk8 epiphyas po |
| 35 | 34 | 70.8 | 137 | 10 Q9SHE5 | Q9she5 arabidopsis |
| 36 | 34 | 70.8 | 157 | 12 Q913W2 | Q913w2 human papil |
| 37 | 34 | 70.8 | 157 | 12 Q913W4 | Q913w4 human papil |
| 38 | 34 | 70.8 | 157 | 12 Q913W5 | Q913w5 human papil |
| 39 | 34 | 70.8 | 157 | 12 Q81962 | Q81962 human papil |
| 40 | 34 | 70.8 | 157 | 12 Q913V9 | Q913v9 human papil |
| 41 | 34 | 70.8 | 157 | 12 Q913W0 | Q913w0 human papil |
| 42 | 34 | 70.8 | 157 | 12 Q913W6 | Q913w6 human papil |
| 43 | 34 | 70.8 | 157 | 12 Q913V8 | Q913v8 human papil |
| 44 | 34 | 70.8 | 157 | 12 Q913V7 | Q913v7 human papil |
| 45 | 34 | 70.8 | 157 | 12 Q81985 | Q81985 human papil |

ALIGNMENTS

RESULT 1

Q8HUW9 ID Q8HUW9 PRELIMINARY; PRT; 366 AA.
AC Q8HUW9;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE NADH dehydrogenase (Fragment).
GN NDHF.
OS Ulmus americana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Rosales; Ulmaceae; Ulmus.
OX NCBI_TaxID=29740;
RN [1]
RP SEQUENCE FROM N.A.
RA Sytsma K.J., Morawetz J., Pires J.C., Nepokroeff M., Conti E.,
RA Zjhra M., Hall J.C., Chase M.W.;
RT "Urticalean rosids: circumscription, rosid ancestry, and phylogenetics
RI based on rbcL, trnL-F, and ndhF sequences.";
RL Am. J. Bot. 89:1531-1546(2002).
DR EMBL: AF500365; AAN63301.1; -;
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 366 366
SQ SEQUENCE: 366 AA; 41953 MW; 4A74694C0B1073EC CRC64;

Query Match 83.3%; Score 40; DB 8; Length 366;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9

Db 307 KKIQLWPK 315

RESULT 2

Q8BQ23

| | | | | |
|--|--|--------------|---------|---------|
| ID | Q8BQ23 | PRELIMINARY; | PRT; | 701 AA. |
| AC | Q8BQ23; | | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23, Created) | | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) | | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) | | | |
| DE | Adenosine deaminase 3. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=C57BL/6J; TISSUE=Brain; | | | |
| RX | MEDLINE=22354683; PubMed=12466851; | | | |
| RA | The FANTOM Consortium, | | | |
| RA | the RIKEN Genome Exploration Research Group Phase I & II Team; | | | |
| RT | *Analysis of the mouse transcriptome based on functional annotation of | | | |
| RT | 60,770 full-length cDNAs.*; | | | |
| RL | Nature 420:563-573(2002). | | | |
| DR | EMBL; AK046083; BAC32597.1; -. | | | |
| SQ | SEQUENCE 701 AA; 77260 MW; E9B076EF9BCF58E2 CRC64; | | | |
| Query Match 81.2%; Score 39; DB 11; Length 701; | | | | |
| Best Local Similarity 75.0%; Pred. No. 35; | | | | |
| Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0; | | | | |
| QY | 2 KQILWK 9 | | | |
| | | | | |
| Db | 112 KQILWK 119 | | | |
| RESULT 3 | | | | |
| Q9JIE5 | PRELIMINARY; | PRT; | 731 AA. | |
| ID | Q9JIE5 | | | |
| AC | Q9JIE5; | | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Created) | | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) | | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) | | | |
| DE | RNA adenosine deaminase RED2 (Fragment). | | | |
| GN | ADAR3. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Brain; | | | |
| RX | MEDLINE=20314475; PubMed=10854777; | | | |
| RA | Slavov D., Clark M., Gardiner K.; | | | |
| RT | *Comparative analysis of the RED1 and RED2 A-to-I RNA editing genes | | | |
| RT | from mammals, pufferfish and zebrafish.*; | | | |
| RL | Gene 250:41-51(2000). | | | |
| DR | EMBL; AF232942; AAF78580.1; -. | | | |
| DR | MGD; MGI:2151118; Adar3. | | | |
| DR | InterPro; IPR001159; A_deamin. | | | |
| DR | InterPro; IPR001159; DS_RBD. | | | |
| DR | Pfam; PF02137; A_deamin; 1. | | | |
| DR | Pfam; PF00035; dsrm; 2. | | | |
| DR | SMART; SM00552; ADEAMC; 1. | | | |
| DR | SMART; SM00358; DSRM; 2. | | | |
| DR | PROSITE; PS50141; A_DEAMIN_EDITASE; 1. | | | |
| DR | PROSITE; PS50137; DS_RBD; 2. | | | |
| FT | NON_TER 1 | | | |
| FT | NON_TER 731 | | | |
| SQ | SEQUENCE 731 AA; 80857 MW; B2F8CBE179BF4A89 CRC64; | | | |
| Query Match 81.2%; Score 39; DB 11; Length 731; | | | | |
| Best Local Similarity 75.0%; Pred. No. 37; | | | | |
| Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0; | | | | |
| QY | 2 KQILWK 9 | | | |
| | | | | |
| Db | 102 KQILWK 109 | | | |

| | | | | |
|--|--|------|---------|--|
| RESULT 4 | | | | |
| Q9JI20 | PRELIMINARY; | PRT; | 745 AA. | |
| ID | Q9JI20 | | | |
| AC | Q9JI20; | | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Created) | | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) | | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) | | | |
| DE | RNA dependent adenosine deaminase 3. | | | |
| GN | ADAR3. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=C57BL/6J; | | | |
| RA | Chen M.-H., Kabir K., Yang J.-H.; | | | |
| RT | *Editing activity of mouse RED2 (ADAR3) in vitro.*; | | | |
| RL | Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL; AF270495; AAF76894.1; -. | | | |
| DR | MGD; MGI:2151118; Adar3. | | | |
| DR | InterPro; IPR002466; A_deamin. | | | |
| DR | InterPro; IPR001159; DS_RBD. | | | |
| DR | Pfam; PF02137; A_deamin; 1. | | | |
| DR | Pfam; PF00035; dsrm; 2. | | | |
| DR | SMART; SM00552; ADEAMC; 1. | | | |
| DR | SMART; SM00358; DSRM; 2. | | | |
| DR | PROSITE; PS50141; A_DEAMIN_EDITASE; 1. | | | |
| DR | PROSITE; PS50137; DS_RBD; 2. | | | |
| SQ | SEQUENCE 745 AA; 82085 MW; 6F208288F741B7D8 CRC64; | | | |
| Query Match 81.2%; Score 39; DB 11; Length 745; | | | | |
| Best Local Similarity 75.0%; Pred. No. 38; | | | | |
| Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0; | | | | |
| QY | 2 KQILWK 9 | | | |
| | | | | |
| Db | 112 KQILWK 119 | | | |
| RESULT 5 | | | | |
| Q8CC51 | PRELIMINARY; | PRT; | 745 AA. | |
| ID | Q8CC51 | | | |
| AC | Q8CC51; | | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23, Created) | | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) | | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) | | | |
| DE | Adenosine deaminase 3. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=C57BL/6J; TISSUE=Diencephalon; | | | |
| RX | MEDLINE=22354683; PubMed=12466851; | | | |
| RA | The FANTOM Consortium, | | | |
| RA | the RIKEN Genome Exploration Research Group Phase I & II Team; | | | |
| RT | *Analysis of the mouse transcriptome based on functional annotation of | | | |
| RT | 60,770 full-length cDNAs.*; | | | |
| RL | Nature 420:563-573(2002). | | | |
| DR | EMBL; AK033916; BAC28513.1; -. | | | |
| SQ | SEQUENCE 745 AA; 82187 MW; A336473C760902F7 CRC64; | | | |
| Query Match 81.2%; Score 39; DB 11; Length 745; | | | | |
| Best Local Similarity 75.0%; Pred. No. 38; | | | | |
| Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0; | | | | |
| QY | 2 KQILWK 9 | | | |
| | | | | |
| Db | 112 KQILWK 119 | | | |

RESULT 6
P97616
ID P97616 PRELIMINARY; PRT; 746 AA.
AC P97616;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Double-stranded RNA specific adenosine deaminase.
GN RED2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97112965; PubMed=8943218;
RA Melcher T., Maas S., Herb A., Sprengel R., Higuchi M., Seeburg P.H.;
RT "RED2, a brain-specific member of the RNA-specific adenosine deaminase family";
RL J. Biol. Chem. 271:31795-31798(1996).
DR EMBL; U74586; AAB41862.1; -;
DR InterPro; IPR002466; A_deamin.
DR InterPro; IPR001159; DS_RHD.
DR Pfam; PF02137; A_deamin; 1.
DR Pfam; PF00035; dsrm; 2.
DR SMART; SM00552; ADEAMC; 1.
DR SMART; SM00358; DSRM; 2.
DR PROSITE; PS50141; A_DEAMIN_EDITASE; 1.
DR PROSITE; PS50137; DS_RBD; 2.
SQ SEQUENCE 746 AA; 82227 MW; 6741BA5FDA699077 CRC64;
Query Match 81.2%; Score 39; DB 11; Length 746;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 KLQILWKK 9
|||:||||
DB 113 KLQILWKK 120
RESULT 7
Q96BQ3
ID Q96BQ3 PRELIMINARY; PRT; 446 AA.
AC Q96BQ3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; BC015353; AAH15353.1; -;
DR Genew; HGNC:19015; TRIM43.
DR InterPro; IPR001870; B302.
DR InterPro; IPR003877; SPRY_receptor.
DR InterPro; IPR000315; Znf_Bbox.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; zf-R_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.

KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 446 AA; 52265 MW; 805E4AA25617724A CRC64;
Query Match 79.2%; Score 38; DB 4; Length 446;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLQILWKK 9
|||:||||
DB 142 KOMRILWKK 150
RESULT 8
Q9LSS5
ID Q9LSS5 PRELIMINARY; PRT; 564 AA.
AC Q9LSS5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Myosin heavy chain-like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB026632; BAA97502.1; -;
SQ SEQUENCE 564 AA; 63712 MW; 18A9F64BA991F2C9 CRC64;
Query Match 79.2%; Score 38; DB 10; Length 564;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KKLQILWKK 9
|||:||||
DB 553 KKIGVLWKK 561
RESULT 9
Q9NS39
ID Q9NS39 PRELIMINARY; PRT; 739 AA.
AC Q9NS39;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Double-stranded RNA specific adenosine deaminase.
GN ADAR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20294785; PubMed=10836796;
RA Chen C.X., Cho D.S., Wang Q., Lai F., Carter K.C., Nishikura K.;
RT "A third member of the RNA-specific adenosine deaminase gene family, ADAR3, contains both single- and double-stranded RNA binding domains.";
RL RNA 6:755-767(2000).
DR EMBL; AF034837; AAF78094.1; -;
DR InterPro; IPR002466; A_deamin.
DR InterPro; IPR001159; DS_RBD.
DR Pfam; PF02137; A_deamin; 1.
DR Pfam; PF00035; dsrm; 2.
DR SMART; SM00552; ADEAMC; 1.
DR SMART; SM00358; DSRM; 2.
DR PROSITE; PS50141; A_DEAMIN_EDITASE; 1.

DR PROSITE; PS50137; DS_RHD; 2.
SQ SEQUENCE 739 AA; 80621 MW; A158A81D35894F79 CRC64;

Query Match 79.2%; Score 38; DB 4; Length 739;
Best Local Similarity 75.0%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKLQILWKK 9
| | | : | | |
Db 112 KKLQVWKK 119

RESULT 10
Q8I634 PRELIMINARY; PRT; 900 AA.
AC Q8I634;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Protein with DNAJ domain (resa-like), putative.
GN PFL0055C.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=2255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014844; AAN36100.1; -.
SQ SEQUENCE 900 AA; 107626 MW; AE90E2273E85FCAA CRC64;

Query Match 79.2%; Score 38; DB 5; Length 900;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
| | | : | | |
Db 181 KKLQVWKK 189

RESULT 11
Q8JNA1 PRELIMINARY; PRT; 148 AA.
AC Q8JNA1;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Putative transforming protein E6.
GN E6.
OS Human papillomavirus type 9C.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=202251;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22079881; PubMed=12085327;
RA Terai M., Burk R.D.;
RT "Identification and Characterization of 3 Novel Genital Human
RT Papillomaviruses by Overlapping Polymerase Chain Reaction: candHPV89,
RT candHPV90, and candHPV91.";
RL J. Infect. Dis. 185:1794-1797(2002).

RN [2]
RP SEQUENCE FROM N.A.
RA Burk R.D., Terai M.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY057438; AAL14204.1; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR001334; E6.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00518; E6; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00213; LIPOCALIN; 1.
SQ SEQUENCE 148 AA; 17173 MW; 374D44C7D05C95DA CRC64;

Query Match 77.1%; Score 37; DB 12; Length 148;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
| | | : | | |
Db 47 KKLQVWKK 55

RESULT 12
Q9BUW4 PRELIMINARY; PRT; 208 AA.
AC Q9BUW4;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; BC001862; AAH01862.1; -.
DR Genew; HGNC:19021; TRIM48.
DR InterPro; IPR000315; Znf_Bbox.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50119; ZF_BBOX; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 208 AA; 24497 MW; 93DD7840775F6E57 CRC64;

Query Match 75.0%; Score 36; DB 4; Length 208;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
| | | : | | |
Db 142 KKLQSLWEK 150

RESULT 13
Q8XMB9 PRELIMINARY; PRT; 279 AA.
AC Q8XMB9;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Probable transcriptional regulator.
GN CPE0770.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT *Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.*;
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL: AP003188; BAB80476.1; -.
DR InterPro: IPR000005; HTHARAC.
DR Pfam: PF00165; HTH_Arac; 2.
DR PRINTS: PR00032; HTHARAC.
DR SMART: SM00342; HTH_ARAC; 1.
DR PROSITE: PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE: PS01124; HTH_ARAC_FAMILY_2; 1.
KW Complete proteome.
SQ SEQUENCE 279 AA; 32341 MW; F511D10D89D409E4 CRC64;

Query Match 75.0%; Score 36; DB 16; Length 279;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LQILWKK 9
:|||||
Db 1 MQILWKK 7

RESULT 14

Q8IWZ4
ID Q8IWZ4 PRELIMINARY; PRT; 375 AA.
AC Q8IWZ4;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Tripartite motif protein 48.
GN TRIM48.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Meroni G.;
RT *Novel tripartite motif family members.*;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF521869; AA014946.1; -.
SQ SEQUENCE 375 AA; 43408 MW; 03C69CH0453C2FD8 CRC64;

Query Match 75.0%; Score 36; DB 4; Length 375;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
||:| ||:|
Db 142 KKMOSLWEX 150

RESULT 15

Q8K5B1
ID Q8K5B1 PRELIMINARY; PRT; 716 AA.
AC Q8K5B1;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Gpl30-like monocyte receptor.
GN GLMR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21988187; PubMed=11877449;
RA Ghilardi N., Li J., Hongo J.A., Yi S., Gurney A., De Sauvage F.J.;
RT *A Novel Type I Cytokine Receptor Is Expressed on Monocytes, Signals
RT Proliferation, and Activates STAT-3 and STAT-5.*;
RL J. Biol. Chem. 277:16831-16836(2002).
DR EMBL: AF486621; AAM27959.1; -.
DR MGD: MGI:2180511; Glmr.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 3.
KW Receptor.
SQ SEQUENCE 716 AA; 80641 MW; 39E6B0B253F7C7E5 CRC64;

Query Match 75.0%; Score 36; DB 11; Length 716;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQILWKK 9
:||:|||||
Db 231 RKVRLWKK 239

Search completed: October 14, 2003, 14:36:58
Job time : 32.8125 secs

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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:19 ; Search time 38.625 Seconds
(without alignments)
36.985 Million cell updates/sec

Title: US-09-881-490-164
Perfect score: 48
Sequence: 1 KKWLIQIKK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query | | | DB ID | Description |
|------------|-------|-------|--------|-------|-------------|
| | Score | Match | Length | | |
| 1 | 48 | 100.0 | 9 | 17 | AAW04030 |
| 2 | 48 | 100.0 | 9 | 18 | AAW44559 |
| 3 | 48 | 100.0 | 9 | 18 | AAW44561 |
| 4 | 48 | 100.0 | 9 | 18 | AAW44563 |
| 5 | 48 | 100.0 | 9 | 18 | AAW44572 |
| 6 | 48 | 100.0 | 9 | 18 | AAW43753 |
| 7 | 48 | 100.0 | 9 | 18 | AAW43749 |
| 8 | 48 | 100.0 | 9 | 20 | AAW00536 |
| 9 | 48 | 100.0 | 9 | 20 | AAW00538 |

| | | | | | | |
|----|----|-------|----|----|----------|--------------------|
| 10 | 48 | 100.0 | 9 | 20 | AAW00540 | Antifungal peptide |
| 11 | 48 | 100.0 | 9 | 20 | AAW00549 | Antifungal peptide |
| 12 | 48 | 100.0 | 9 | 21 | AAW88384 | Antifungal peptide |
| 13 | 48 | 100.0 | 9 | 22 | AAW65460 | Anti-fungal peptid |
| 14 | 48 | 100.0 | 9 | 22 | AAW65462 | Anti-fungal peptid |
| 15 | 48 | 100.0 | 9 | 22 | AAW65464 | Anti-fungal peptid |
| 16 | 48 | 100.0 | 9 | 22 | AAW65473 | Anti-fungal peptid |
| 17 | 48 | 100.0 | 10 | 17 | AAW04039 | Antifungal peptide |
| 18 | 48 | 100.0 | 10 | 17 | AAW04040 | Antifungal peptide |
| 19 | 48 | 100.0 | 10 | 18 | AAW44578 | Anti-fungal peptid |
| 20 | 48 | 100.0 | 10 | 18 | AAW44579 | Anti-fungal peptid |
| 21 | 48 | 100.0 | 10 | 18 | AAW43761 | Antifungal peptide |
| 22 | 48 | 100.0 | 10 | 18 | AAW43760 | Bactericidal/perme |
| 23 | 48 | 100.0 | 10 | 20 | AAW00555 | Bactericidal/perme |
| 24 | 48 | 100.0 | 10 | 20 | AAW00556 | Antifungal peptide |
| 25 | 48 | 100.0 | 10 | 22 | AAW65479 | Antifungal peptide |
| 26 | 48 | 100.0 | 10 | 22 | AAW65480 | Anti-fungal peptid |
| 27 | 48 | 100.0 | 11 | 17 | AAW04041 | Antifungal peptide |
| 28 | 48 | 100.0 | 11 | 18 | AAW44580 | Anti-fungal peptid |
| 29 | 48 | 100.0 | 11 | 18 | AAW43762 | Bactericidal/perme |
| 30 | 48 | 100.0 | 11 | 20 | AAW00557 | Antifungal peptide |
| 31 | 48 | 100.0 | 11 | 22 | AAW65481 | Antifungal peptide |
| 32 | 43 | 89.6 | 8 | 17 | AAW04027 | Antifungal peptide |
| 33 | 43 | 89.6 | 8 | 17 | AAW04029 | Antifungal peptide |
| 34 | 43 | 89.6 | 8 | 18 | AAW44556 | Anti-fungal peptid |
| 35 | 43 | 89.6 | 8 | 18 | AAW44558 | Anti-fungal peptid |
| 36 | 43 | 89.6 | 8 | 18 | AAW43748 | Bactericidal/perme |
| 37 | 43 | 89.6 | 8 | 20 | AAW00535 | Antifungal peptide |
| 38 | 43 | 89.6 | 8 | 20 | AAW00533 | Antifungal peptide |
| 39 | 43 | 89.6 | 8 | 22 | AAW65457 | Anti-fungal peptid |
| 40 | 43 | 89.6 | 8 | 22 | AAW65459 | Anti-fungal peptid |
| 41 | 43 | 89.6 | 9 | 17 | AAW04031 | Antifungal peptide |
| 42 | 43 | 89.6 | 9 | 17 | AAW04036 | Antifungal peptide |
| 43 | 43 | 89.6 | 9 | 17 | AAW04037 | Antifungal peptide |
| 44 | 43 | 89.6 | 9 | 18 | AAW44564 | Anti-fungal peptid |
| 45 | 43 | 89.6 | 9 | 18 | AAW44565 | Anti-fungal peptid |

ALIGNMENTS

RESULT 1
AAW04030
ID AAW04030 standard; peptide; 9 AA.
XX
AC AAW04030;
XX
DT 04-NOV-1996 (first entry)
XX
DE Antifungal peptide XMP.327/XMP.331/XMP.333/XMP.342.
XX
KW Antifungal peptide; inhibitor; Domain III; polymorphonuclear leukocyte;
KW bactericidal/permeability-increasing protein; BPI; mammalian; PMN; fungi;
KW neutrophil; replication inhibitor; fungal infection; Aspergillus;
KW Cryptococcus; Candida; C.albicans; C.galabrati; C.krusei; C.lusitanae;
KW C.parapsilosis; C.tropicalis; therapy.
XX
OS Synthetic.
XX

| Key | Location/Qualifiers | |
|-----|---------------------|---|
| | Modified-site 1 | /note= "optionally acetylated, optionally D-form residue" |
| FT | Misc-difference 2 | /note= "optionally D-form residue" |
| FT | Misc-difference 8 | /note= "optionally D-form residue" |
| FT | Misc-difference 9 | /note= "amided, optionally D-form residue" |
| PN | WO9608509-A1. | |
| XX | 21-MAR-1996. | |

PF 20-JUL-1995; 95WO-US09262.
XX
PR 13-JAN-1995; 95US-0372105.
PR 15-SEP-1994; 94US-0306473.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;
XX
DR WPI; 1996-179900/18.
XX
PT Antifungal peptide(s) derived from Domain III of BPI protein - used
PT in vitro for killing or inhibiting replication of fungi, esp.
PT Candida species
XX
PS Claim 5; Page 154; 199pp; English.
XX
CC AAW04000-W04160 represent antifungal peptides. These sequences are
CC based on (or derived from) Domain III of the
CC bactericidal/permeability-increasing protein (BPI). BPI is a protein
CC that can be isolated from the granules of mammalian polymorphonuclear
CC leukocytes (PMNs or neutrophils). These antifungal peptides can be used
CC for killing, or inhibiting replication of, fungi in vitro. These
CC sequences can also be used for treatment of a fungal infection involving
CC fungi from the species Candida, Aspergillus and Cryptococcus. The
CC sequences are especially useful for treating C.albicans, C.galabrat,
CC C.krusei, C.lusitaniae, C.parapsilosis and C.tropicalis infections.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLIQLKK 9
Db | | | | | | | | | |
1 KKWLIQLKK 9

RESULT 2
AAW44559
ID AAW44559 standard; peptide; 9 AA.
XX
AC AAW44559;
XX
DT 27-APR-1998 (first entry)
XX
DE Anti-fungal peptide #160 based on BPI protein (residues 142-169).
XX
KW Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.
XX
OS Synthetic.
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Modified-site 9 /note= "C-terminal amide"
FT Modified-site 9 /note= "C-terminal amide"
FT
XX
PN W09704008-A1.
XX
PD 06-FEB-1997.
XX
PF 21-MAR-1996; 96WO-US03845.
XX
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;
XX
DR WPI; 1997-132578/12.
XX

PT Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides
XX
PS Claim 1; Page 191; 230pp; English.
XX
CC This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLIQLKK 9
Db | | | | | | | | | |
1 KKWLIQLKK 9

RESULT 3
AAW44561
ID AAW44561 standard; peptide; 9 AA.
XX
AC AAW44561;
XX
DT 27-APR-1998 (first entry)
XX
DE Anti-fungal peptide #162 based on BPI protein (residues 142-169).
XX
KW Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.
XX
OS Synthetic.
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 9 /note= "C-terminal amide"
FT
XX
PN W09704008-A1.
XX
PD 06-FEB-1997.
XX
PF 21-MAR-1996; 96WO-US03845.
XX
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;
XX
DR WPI; 1997-132578/12.
XX
PT Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides
XX
PS Claim 1; Page 192; 230pp; English.
XX
CC This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in

CC decontaminating fluids and sterilising medical and implant devices.

XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
| | | | |
Db 1 KKWLQLKK 9

RESULT 4

AAW44563
ID AAW44563 standard; peptide; 9 AA.

XX
AC AAW44563;

XX 27-APR-1998 (first entry)

XX Anti-fungal peptide #164 based on BPI protein (residues 142-169).

XX Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.

XX Synthetic.
OS Mammalia.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Modified-site 9 /note= "C-terminal amide"

XX WO9704008-A1.

XX 06-FEB-1997.

XX 21-MAR-1996; 96WO-US03845.

XX 20-JUL-1995; 95US-0504841.

XX (XOMA) XOMA CORP.

XX Fadem MB, Lim E, Little RG;

XX WPI; 1997-132578/12.

XX Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides

XX Claim 1; Page 192; 230pp; English.

XX This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.

XX Sequence 9 AA;

Query Match 100.0%; Score 48; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
| | | | |
Db 1 KKWLQLKK 9

RESULT 5

AAW44572
ID AAW44572 standard; peptide; 9 AA.

XX
AC AAW44572;

XX 27-APR-1998 (first entry)

XX Anti-fungal peptide #173 based on BPI protein (residues 142-169).

XX Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.

XX Synthetic.
OS Mammalia.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 8 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

XX WO9704008-A1.

XX 06-FEB-1997.

XX 21-MAR-1996; 96WO-US03845.

XX 20-JUL-1995; 95US-0504841.

XX (XOMA) XOMA CORP.

XX Fadem MB, Lim E, Little RG;

XX WPI; 1997-132578/12.

XX Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides

XX Claim 1; Page 196; 230pp; English.

XX This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.

XX Sequence 9 AA;

Query Match 100.0%; Score 48; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
| | | | |
Db 1 KKWLQLKK 9

RESULT 6

AAW43753
ID AAW43753 standard; peptide; 9 AA.

XX
AC AAW43753;

XX 20-APR-1998 (first entry)

XX DE Bactericidal/permeability increasing peptide XMP.331.
XX KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW bacterial infection; fungicidal; endotoxin; heparin;
KW anglogenesis; fungicidal; recombinant DNA; vector.
XX OS Homo sapiens.
OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 9 /note= "Acetylated"
FT Modified-site 9 /note= "Amidated"
XX WO9735009-A1.
PN 25-SEP-1997.
PD 18-MAR-1997; 97WO-US05287.
XX 22-MAR-1996; 96US-0621803.
XX (XOMA) XOMA CORP.
XX Better MD;
PI WPI; 1997-480215/44.
XX Recombinant production of bactericidal/permeability increasing
PT protein - by expression as a fusion protein in microbial host cells,
PT then cleaving the BPI peptide from the carrier
XX Claim 10; Page 127; 186pp; English.
XX A new recombinant DNA vector construct has been developed which encodes
CC a fusion protein and is suitable for introduction into a bacterial host.
CC The vector comprises: (a) DNA encoding at least one cationic
CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC located between (a) and (b). The present sequence represents a
CC specifically claimed BPI peptide. The peptides have many uses including
CC the treatment of bacterial and fungal infections. BPI peptides also
CC bind to endotoxins and heparin, neutralising their effects. The
CC peptides have further been shown to inhibit anglogenesis (partly due to
CC heparin-binding activity). The fusion proteins have been found to be
CC expressed in large amounts without significant proteolysis, and in some
CC cases are actually secreted from the host cells. This allows the
CC indirect production of anti-microbial BPI peptides in microbial hosts.
XX SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9
RESULT 7
AAW43749
ID AAW43749 standard; peptide; 9 AA.
XX AAW43749;
AC 20-APR-1998 (first entry)
XX Bactericidal/permeability increasing peptide XMP.327.
DE Bactericidal/permeability increasing peptide; BPI; fusion protein;
XX Bactericidal/permeability increasing peptide; BPI; fusion protein;

KW bacterial infection; fungicidal; recombinant DNA; vector.
KW anglogenesis; fungicidal; recombinant DNA; vector.
XX Homo sapiens.
OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 9 /note= "Amidated"
XX WO9735009-A1.
PN 25-SEP-1997.
PD 18-MAR-1997; 97WO-US05287.
XX 22-MAR-1996; 96US-0621803.
XX (XOMA) XOMA CORP.
XX Better MD;
PI WPI; 1997-480215/44.
XX Recombinant production of bactericidal/permeability increasing
PT protein - by expression as a fusion protein in microbial host cells,
PT then cleaving the BPI peptide from the carrier
XX Claim 10; Page 125; 186pp; English.
XX A new recombinant DNA vector construct has been developed which encodes
CC a fusion protein and is suitable for introduction into a bacterial host.
CC The vector comprises: (a) DNA encoding at least one cationic
CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC located between (a) and (b). The present sequence represents a
CC specifically claimed BPI peptide. The peptides have many uses including
CC the treatment of bacterial and fungal infections. BPI peptides also
CC bind to endotoxins and heparin, neutralising their effects. The
CC peptides have further been shown to inhibit anglogenesis (partly due to
CC heparin-binding activity). The fusion proteins have been found to be
CC expressed in large amounts without significant proteolysis, and in some
CC cases are actually secreted from the host cells. This allows the
CC indirect production of anti-microbial BPI peptides in microbial hosts.
XX SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9
RESULT 8
AAW00536
ID AAW00536 standard; Peptide; 9 AA.
XX AAW00536;
AC 07-MAY-1999 (first entry)
XX Antifungal peptide XMP.327.
DE Antifungal; BPI; bactericidal/permeability increasing protein;
KW Candida infection.
XX Synthetic.
XX US5858974-A.
PN XX

PD 12-JAN-1999.
XX
PF 21-MAR-1996; 96US-0621259.
XX
PR 21-MAR-1996; 96US-0621259.
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;
XX
DR WPI; 1999-119956/10.

XX Antifungal peptides - comprising part of bactericidal or
PT permeability-increasing protein sequence or related sequence
PS Disclosure; Columns 165-166; 132pp; English.

XX New peptides are provided which are based on Domain III (amino acids
CC 142-169) of human bactericidal/permeability-increasing protein (BPI).
CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGVLIQLFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, IQLF, WLIQL, LIQLF and WLIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of
CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.

XX Sequence 9 AA;

Query Match 100.0%; Score 48; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLIIQLKK 9
Db | | | | | | | | | |
1 KKWLIIQLKK 9

RESULT 9
AAAY00538
ID AAAY00538 standard; Peptide; 9 AA.

XX
AC AAAY00538;
XX
DT 07-MAY-1999 (first entry)
XX
DE Antifungal peptide XMP.331.
XX
KW Antifungal; BPI; bactericidal/permeability increasing protein;
KW Candida infection.
XX
OS Synthetic.
XX
PN US5858974-A.
XX
PD 12-JAN-1999.
XX
PF 21-MAR-1996; 96US-0621259.

XX
PR 21-MAR-1996; 96US-0621259.
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;

XX WPI; 1999-119956/10.
DR
XX
PT Antifungal peptides - comprising part of bactericidal or
PT permeability-increasing protein sequence or related sequence
XX
PS Disclosure; Columns 165-166; 132pp; English.

XX New peptides are provided which are based on Domain III (amino acids
CC 142-169) of human bactericidal/permeability-increasing protein (BPI).
CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGVLIQLFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, IQLF, WLIQL, LIQLF and WLIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of
CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.

XX Sequence 9 AA;

Query Match 100.0%; Score 48; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLIIQLKK 9
Db | | | | | | | | | |
1 KKWLIIQLKK 9

RESULT 10
AAAY00540
ID AAAY00540 standard; Peptide; 9 AA.

XX
AC AAAY00540;
XX
DT 07-MAY-1999 (first entry)
XX
DE Antifungal peptide XMP.333.
XX
KW Antifungal; BPI; bactericidal/permeability increasing protein;
KW Candida infection.
XX
OS Synthetic.
XX
PN US5858974-A.
XX
PD 12-JAN-1999.
XX
PF 21-MAR-1996; 96US-0621259.

XX
PR 21-MAR-1996; 96US-0621259.
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;
XX
DR WPI; 1999-119956/10.

XX Antifungal peptides - comprising part of bactericidal or
PT permeability-increasing protein sequence or related sequence
XX
PS Disclosure; Columns 167-168; 132pp; English.

XX New peptides are provided which are based on Domain III (amino acids
CC 142-169) of human bactericidal/permeability-increasing protein (BPI).

CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGLIQLFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, IQLF, WLIQL, LIQLF and WLIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of
CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLIQLKK 9
| | | | | | | | |
Db 1 KKWLIQLKK 9

RESULT 11
AAY00549
ID AAY00549 standard; Peptide; 9 AA.
XX
AC AAY00549;
XX
DT 07-MAY-1999 (first entry)
XX
DE Antifungal peptide XMP.342.
XX
KW Antifungal; BPI; bactericidal/permeability increasing protein;
KW Candida infection.
XX
OS Synthetic.
XX US5858974-A.
PN
PD 12-JAN-1999.
XX
PF 21-MAR-1996; 96US-0621259.
XX
PR 21-MAR-1996; 96US-0621259.
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Fadem MB, Lim E, Little RG;
XX
DR WPI: 1999-119956/10.
XX
PT Antifungal peptides - comprising part of bactericidal or
PT permeability-increasing protein sequence or related sequence
XX
PS Disclosure; Columns 173-174; 132pp; English.
XX
CC New peptides are provided which are based on Domain III (amino acids
CC 142-169) of human bactericidal/permeability-increasing protein (BPI).
CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGLIQLFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, IQLF, WLIQL, LIQLF and WLIQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of

CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLIQLKK 9
| | | | | | | | |
Db 1 KKWLIQLKK 9

RESULT 12
AAY88384
ID AAY88384 standard; peptide; 9 AA.
XX
AC AAY88384;
XX
DT 24-JUL-2000 (first entry)
XX
DE Antifungal peptide XMP.342.
XX
KW Antifungal peptide; XMP.342; BPI; microorganism; defence; antibacterial;
KW bactericidal/permeability increasing protein; antimicrobial; XMP. 445;
KW fungal infection; Candida; Aspergillus; Fusarium; growth inhibitor;
KW decontaminate; sterilize; medical equipment; prosthetic joint.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Misc-difference 2 /note= "D-form residue"
FT Misc-difference 8 /note= "D-form residue"
FT Modified-site 9 /note= "D-form residue, C-terminal amide"
FT
FT
PN WO200018798-A1.
XX
XX
PD 06-APR-2000.
XX
PF 24-SEP-1999; 99WO-US22277.
XX
PR 25-SEP-1998; 98US-0101958.
PR 25-NOV-1998; 98US-0109896.
XX
PA (XOMA) XOMA TECHNOLOGY LTD.
XX
PI Little RG;
XX
DR WPI: 2000-303442/26.
XX
PT A new antifungal peptide, designated XMP.445, used to treat fungal
PT infections is based on Domain III of
PT bactericidal/permeability-increasing protein -
XX
PS Example 2; Page 28; 31pp; English.
XX
CC This sequence represents an antifungal peptide designated XMP.342, which
CC is based on amino acids 153-157 of bactericidal/permeability increasing
CC (BPI) protein (see AAY88382). BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or neutrophils),
CC which are essential in the defence against invading microorganisms. BPI
CC protein products have antibacterial and antimicrobial activity. The
CC invention relates to antibacterial peptides, specifically XMP.445 (see
CC AAY88381). The peptide is used to treat fungal infections, particularly
CC infections of the species Candida, Aspergillus or Fusarium. The peptide

CC can also be used to treat a bacterial infection, or to kill or inhibit
CC the growth of bacteria in vitro. The peptide may be useful to treat
CC animals or plants in vivo, and as an agent to decontaminate fluids and
CC surfaces and to sterilize surgical or other medical equipment and
CC implantable devices including prosthetic joints.

XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 13
AAB65460
ID AAB65460 standard; Peptide; 9 AA.
XX
AC AAB65460;
XX 27-MAR-2001 (first entry)
XX Anti-fungal peptide XMP.327.
XX Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;
KW bactericidal/permeability-increasing protein; bactericidal;
KW fungal infection.
XX Homo sapiens.
XX US6156730-A.
XX 05-DEC-2000.
XX 08-JAN-1999; 99US-0227659.
XX 21-MAR-1996; 96US-0621259.
PR 12-MAR-1993; 93US-0030644.
PR 15-JUL-1993; 93US-0093202.
PR 14-JAN-1994; 94US-0183222.
PR 11-MAR-1994; 94US-0209762.
PR 11-JUL-1994; 94US-0273540.
PR 15-SEP-1994; 94US-0306473.
PR 13-JAN-1995; 95US-0372105.
PR 20-JUL-1995; 95US-0504841.
XX (XOMA) XOMA CORP.
XX Lim E, Fadem MB, Little RG;
XX WPI; 2001-090160/10.
XX Novel anti-fungal peptides derived from domain III of
PT bactericidal/permeability-increasing protein useful for killing or
PT inhibiting replication of fungi and for treating fungal infections -
XX Example 2; Columns 169-170; 134pp; English.
XX The present invention relates to antifungal peptides (see
CC AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C.albicans, C.glabrata, C.krusei,
CC C.lusitanae, C.parapsilosis and C.tropicalis.

SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 14
AAB65462
ID AAB65462 standard; Peptide; 9 AA.
XX
AC AAB65462;
XX 27-MAR-2001 (first entry)
XX Anti-fungal peptide XMP.331.
XX Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;
KW bactericidal/permeability-increasing protein; bactericidal;
KW fungal infection.
XX Homo sapiens.
XX US6156730-A.
XX 05-DEC-2000.
XX 08-JAN-1999; 99US-0227659.
XX 21-MAR-1996; 96US-0621259.
PR 12-MAR-1993; 93US-0030644.
PR 15-JUL-1993; 93US-0093202.
PR 14-JAN-1994; 94US-0183222.
PR 11-MAR-1994; 94US-0209762.
PR 11-JUL-1994; 94US-0273540.
PR 15-SEP-1994; 94US-0306473.
PR 13-JAN-1995; 95US-0372105.
PR 20-JUL-1995; 95US-0504841.
XX (XOMA) XOMA CORP.
XX Lim E, Fadem MB, Little RG;
XX WPI; 2001-090160/10.
XX Novel anti-fungal peptides derived from domain III of
PT bactericidal/permeability-increasing protein useful for killing or
PT inhibiting replication of fungi and for treating fungal infections -
XX Example 2; Columns 171-172; 134pp; English.
XX The present invention relates to antifungal peptides (see
CC AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C.albicans, C.glabrata, C.krusei,
CC C.lusitanae, C.parapsilosis and C.tropicalis.

XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Job time : 38.7917 secs

QY 1 KKWLQLKK 9
| | | | | | | |
Db 1 KKWLQLKK 9

RESULT 15
AAB65464
ID AAB65464 standard; Peptide; 9 AA.
XX
AC AAB65464;
XX
DT 27-MAR-2001 (first entry)
XX
DE Anti-fungal peptide XMP.333.
XX
KW Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;
KW bactericidal/permeability-increasing protein; bactericidal;
KW fungal infection.
XX
OS Homo sapiens.
XX
PN US6156730-A.
XX
PD 05-DEC-2000.
XX
PF 08-JAN-1999; 99US-0227659.
XX
PR 21-MAR-1996; 96US-0621259.
PR 12-MAR-1993; 93US-0030644.
PR 15-JUL-1993; 93US-0093202.
PR 14-JAN-1994; 94US-0183222.
PR 11-MAR-1994; 94US-0209762.
PR 11-JUL-1994; 94US-0273540.
PR 15-SEP-1994; 94US-0306473.
PR 13-JAN-1995; 95US-0372105.
PR 20-JUL-1995; 95US-0504841.

XX (XOMA) XOMA CORP.
XX
PI Lim E, Fadem MR, Little RG;
XX
DR WPI; 2001-090160/10.
XX
PT Novel anti-fungal peptides derived from domain III of
PT bactericidal/permeability-increasing protein: useful for killing or
PT inhibiting replication of fungi and for treating fungal infections -
XX
PS Example 2; Columns 173-174; 134pp; English.
XX
CC The present invention relates to antifungal peptides (see
CC AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C.albicans, C.glabrata, C.krusei,
CC C.lusitanae, C.parapsilosis and C.tropicalis.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DH 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
| | | | | | | |
Db 1 KKWLQLKK 9

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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:23 ; Search time 12.75 Seconds
(without alignments)
29.866 Million cell updates/sec

Title: US-09-881-490-164
Perfect score: 48
Sequence: 1 KKWLQIKK 9

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Searched: 328717 seqs, 42310853 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 48 | 100.0 | 9 | 2 | US-08-621-803-193 Sequence 193, App |
| 2 | 48 | 100.0 | 9 | 2 | US-08-621-803-197 Sequence 197, App |
| 3 | 48 | 100.0 | 9 | 2 | US-08-621-259A-160 Sequence 160, App |
| 4 | 48 | 100.0 | 9 | 2 | US-08-621-259A-162 Sequence 162, App |
| 5 | 48 | 100.0 | 9 | 2 | US-08-621-259A-164 Sequence 164, App |
| 6 | 48 | 100.0 | 9 | 2 | US-08-621-259A-173 Sequence 173, App |
| 7 | 48 | 100.0 | 9 | 3 | US-09-217-352-193 Sequence 193, App |
| 8 | 48 | 100.0 | 9 | 3 | US-09-217-352-197 Sequence 197, App |
| 9 | 48 | 100.0 | 9 | 5 | PCT-US95-09262-160 Sequence 160, App |
| 10 | 48 | 100.0 | 9 | 5 | PCT-US95-09262-162 Sequence 162, App |
| 11 | 48 | 100.0 | 9 | 5 | PCT-US95-09262-164 Sequence 164, App |
| 12 | 48 | 100.0 | 9 | 5 | PCT-US95-09262-173 Sequence 173, App |
| 13 | 48 | 100.0 | 10 | 2 | US-08-621-803-204 Sequence 204, App |
| 14 | 48 | 100.0 | 10 | 2 | US-08-621-803-205 Sequence 205, App |
| 15 | 48 | 100.0 | 10 | 2 | US-08-621-259A-179 Sequence 179, App |
| 16 | 48 | 100.0 | 10 | 2 | US-08-621-259A-180 Sequence 180, App |
| 17 | 48 | 100.0 | 10 | 3 | US-09-217-352-204 Sequence 204, App |
| 18 | 48 | 100.0 | 10 | 3 | US-09-217-352-205 Sequence 205, App |
| 19 | 48 | 100.0 | 10 | 5 | PCT-US95-09262-179 Sequence 179, App |
| 20 | 48 | 100.0 | 10 | 5 | PCT-US95-09262-180 Sequence 180, App |
| 21 | 48 | 100.0 | 11 | 2 | US-08-621-803-206 Sequence 206, App |
| 22 | 48 | 100.0 | 11 | 2 | US-08-621-259A-181 Sequence 181, App |
| 23 | 48 | 100.0 | 11 | 3 | US-09-217-352-206 Sequence 206, App |
| 24 | 48 | 100.0 | 11 | 5 | PCT-US95-09262-181 Sequence 181, App |
| 25 | 43 | 89.6 | 8 | 2 | US-08-621-803-192 Sequence 192, App |
| 26 | 43 | 89.6 | 8 | 2 | US-08-621-259A-157 Sequence 157, App |
| 27 | 43 | 89.6 | 8 | 2 | US-08-621-259A-159 Sequence 159, App |

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| 28 | 43 | 89.6 | 8 | 3 | US-09-217-352-192 Sequence 192, App |
| 29 | 43 | 89.6 | 8 | 5 | PCT-US95-09262-157 Sequence 157, App |
| 30 | 43 | 89.6 | 8 | 5 | PCT-US95-09262-159 Sequence 159, App |
| 31 | 43 | 89.6 | 9 | 2 | US-08-621-803-198 Sequence 198, App |
| 32 | 43 | 89.6 | 9 | 2 | US-08-621-803-202 Sequence 202, App |
| 33 | 43 | 89.6 | 9 | 2 | US-08-621-803-203 Sequence 203, App |
| 34 | 43 | 89.6 | 9 | 2 | US-08-621-259A-165 Sequence 165, App |
| 35 | 43 | 89.6 | 9 | 2 | US-08-621-259A-166 Sequence 166, App |
| 36 | 43 | 89.6 | 9 | 2 | US-08-621-259A-175 Sequence 175, App |
| 37 | 43 | 89.6 | 9 | 2 | US-08-621-259A-176 Sequence 176, App |
| 38 | 43 | 89.6 | 9 | 2 | US-08-621-259A-206 Sequence 206, App |
| 39 | 43 | 89.6 | 9 | 2 | US-08-621-259A-241 Sequence 241, App |
| 40 | 43 | 89.6 | 9 | 2 | US-08-621-259A-242 Sequence 242, App |
| 41 | 43 | 89.6 | 9 | 3 | US-09-217-352-198 Sequence 198, App |
| 42 | 43 | 89.6 | 9 | 3 | US-09-217-352-202 Sequence 202, App |
| 43 | 43 | 89.6 | 9 | 3 | US-09-217-352-203 Sequence 203, App |
| 44 | 43 | 89.6 | 9 | 5 | PCT-US95-09262-165 Sequence 165, App |
| 45 | 43 | 89.6 | 9 | 5 | PCT-US95-09262-166 Sequence 166, App |

ALIGNMENTS

RESULT 1
US-08-621-803-193
; Sequence 193, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; FUSION PROTEINS AND DERIVED PEPTIDES
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.327"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."

Query Match 100.0%; Score 48; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWL1QLKK 9
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Db 1 KKWL1QLKK 9

RESULT 2
US-08-621-803-197
; Sequence 197, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621.803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 197:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.331"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetylated
; OTHER INFORMATION: /note= "Position 1 is acetylated."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-803-197

Query Match 100.0%; Score 48; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWL1QLKK 9
   |||||
Db 1 KKWL1QLKK 9

RESULT 3
US-08-621-259A-160
; Sequence 160, Application US/08621259A
; Patent No. 5858974
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; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621.259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 110210502
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.327"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-160

Query Match 100.0%; Score 48; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWL1QLKK 9
   |||||
Db 1 KKWL1QLKK 9

RESULT 4
US-08-621-259A-162
; Sequence 162, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
```



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/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: misc_feature
/ OTHER INFORMATION: "XMP.331"
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 1
/ OTHER INFORMATION: /label= Acetylated
/ OTHER INFORMATION: /note= "Position 1 is acetylated"
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: C-Terminus
/ OTHER INFORMATION: /label= Amidation
/ OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-162

Query Match          100.0%; Score 48; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKWLQLKK 9
Db      1 KKWLQLKK 9

RESULT 11
PCT-US95-09262-164
; Sequence 164, Application PC/TUS9509262
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09262
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/10040
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/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/474-6300
/ TELEFAX: 312/474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 164:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: misc_feature
/ OTHER INFORMATION: "XMP.333"
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 1
/ OTHER INFORMATION: /label= D-Lys
/ OTHER INFORMATION: /note= "Position 1 is D-lysine"
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: C-Terminus
/ OTHER INFORMATION: /label= Amidation
/ OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-164

Query Match          100.0%; Score 48; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKWLQLKK 9
Db      1 KKWLQLKK 9

RESULT 12
PCT-US95-09262-173
; Sequence 173, Application PC/TUS9509262
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09262
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/093,202
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;
; FILING DATE: 15-JUL-93
; PRIOR APPLICATION DATA: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION/DOCKET NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/10040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 173:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.342"
;
; NAME/KEY: Modified-site
; LOCATION: 1, 2, 8 & 9
; OTHER INFORMATION: /label= D-Lys
; OTHER INFORMATION: /note= "Positions 1, 2, 8 & 9 are D-lysine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-173

Query Match 100.0%; Score 48; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
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Db 1 KKWLQLKK 9

RESULT 13
US-08-621-803-204
; Sequence 204, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448

;
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 204:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.348"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-803-204

Query Match 100.0%; Score 48; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
| | | | | | | |
Db 2 KKWLQLKK 10

RESULT 14
US-08-621-803-205
; Sequence 205, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.349"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-803-205

Query Match 100.0%; Score 48; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 15
US-08-621-259A-179
; Sequence 179, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger C
; APPLICANT: Lim, Edward
; APPLICANT: Faden, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 179:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.348"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-179

Query Match 100.0%; Score 48; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
Db 2 KKWLQLKK 10

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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:34:14 ; Search time 21.9375 Seconds
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Title: US-09-881-490-164
Perfect score: 48
Sequence: 1 KKWLQLKK 9

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Post-processing: Minimum Match 0%
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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 48 | 100.0 | 9 | 9 | US-09-765-527-197 |
| 3 | 48 | 100.0 | 9 | 9 | US-09-881-490-160 |
| 4 | 48 | 100.0 | 9 | 9 | US-09-881-490-162 |
| 5 | 48 | 100.0 | 9 | 9 | US-09-881-490-164 |
| 6 | 48 | 100.0 | 9 | 9 | US-09-881-490-173 |
| 7 | 48 | 100.0 | 10 | 9 | US-09-765-527-204 |
| 8 | 48 | 100.0 | 10 | 9 | US-09-765-527-205 |
| 9 | 48 | 100.0 | 10 | 9 | US-09-881-490-179 |
| 10 | 48 | 100.0 | 10 | 9 | US-09-881-490-180 |
| 11 | 48 | 100.0 | 11 | 9 | US-09-765-527-206 |
| 12 | 48 | 100.0 | 11 | 9 | US-09-881-490-181 |
| 13 | 43 | 89.6 | 8 | 9 | US-09-765-527-192 |
| 14 | 43 | 89.6 | 8 | 9 | US-09-881-490-157 |
| 15 | 43 | 89.6 | 8 | 9 | US-09-881-490-159 |

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| 16 | 43 | 89.6 | 9 | 9 | US-09-765-527-198 | Sequence 198, App |
| 17 | 43 | 89.6 | 9 | 9 | US-09-765-527-202 | Sequence 202, App |
| 18 | 43 | 89.6 | 9 | 9 | US-09-765-527-203 | Sequence 203, App |
| 19 | 43 | 89.6 | 9 | 9 | US-09-881-490-165 | Sequence 165, App |
| 20 | 43 | 89.6 | 9 | 9 | US-09-881-490-166 | Sequence 166, App |
| 21 | 43 | 89.6 | 9 | 9 | US-09-881-490-175 | Sequence 175, App |
| 22 | 43 | 89.6 | 9 | 9 | US-09-881-490-176 | Sequence 176, App |
| 23 | 43 | 89.6 | 10 | 9 | US-09-765-527-216 | Sequence 216, App |
| 24 | 40 | 83.3 | 10 | 9 | US-09-765-527-207 | Sequence 207, App |
| 25 | 40 | 83.3 | 10 | 9 | US-09-881-490-182 | Sequence 182, App |
| 26 | 38 | 79.2 | 7 | 9 | US-09-765-527-188 | Sequence 188, App |
| 27 | 38 | 79.2 | 7 | 9 | US-09-765-527-189 | Sequence 189, App |
| 28 | 38 | 79.2 | 7 | 9 | US-09-765-527-190 | Sequence 190, App |
| 29 | 38 | 79.2 | 7 | 9 | US-09-765-527-191 | Sequence 191, App |
| 30 | 38 | 79.2 | 7 | 9 | US-09-881-490-155 | Sequence 155, App |
| 31 | 38 | 79.2 | 7 | 9 | US-09-881-490-156 | Sequence 156, App |
| 32 | 38 | 79.2 | 7 | 9 | US-09-881-490-158 | Sequence 158, App |
| 33 | 38 | 79.2 | 9 | 9 | US-09-765-527-236 | Sequence 236, App |
| 34 | 38 | 79.2 | 9 | 9 | US-09-881-490-177 | Sequence 177, App |
| 35 | 38 | 79.2 | 10 | 9 | US-09-765-527-214 | Sequence 214, App |
| 36 | 38 | 79.2 | 11 | 9 | US-09-765-527-208 | Sequence 208, App |
| 37 | 38 | 79.2 | 11 | 9 | US-09-881-490-183 | Sequence 183, App |
| 38 | 38 | 79.2 | 11 | 9 | US-09-881-490-189 | Sequence 189, App |
| 39 | 37 | 77.1 | 10 | 9 | US-09-765-527-218 | Sequence 218, App |
| 40 | 36 | 75.0 | 9 | 9 | US-09-765-527-199 | Sequence 199, App |
| 41 | 36 | 75.0 | 9 | 9 | US-09-881-490-167 | Sequence 167, App |
| 42 | 36 | 75.0 | 436 | 10 | US-09-925-300-1640 | Sequence 1640, Ap |
| 43 | 35 | 72.9 | 55 | 11 | US-09-764-891-3233 | Sequence 3233, Ap |
| 44 | 35 | 72.9 | 2073 | 11 | US-09-978-244A-10 | Sequence 10, Appl |
| 45 | 34 | 70.8 | 9 | 9 | US-09-765-527-201 | Sequence 201, App |

ALIGNMENTS

RESULT 1
US-09-765-527-193
; Sequence 193, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.327"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-09-765-527-193

Query Match 100.0%; Score 48; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. NO. 5.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLIQLKK 9
Db 1 KKWLIQLKK 9

RESULT 2
US-09-765-527-197
; Sequence 197, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 197:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.331"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetylated
; /note= "Position 1 is acetylated."
; FEATURE:
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; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 197:
US-09-765-527-197

Query Match 100.0%; Score 48; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. NO. 5.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLIQLKK 9
Db 1 KKWLIQLKK 9

RESULT 3
US-09-881-490-160
; Sequence 160, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
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; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.327"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 160:
US-09-881-490-160

Query Match      100.0%; Score 48; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. NO. 5.4e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKWLQLKK 9
Db      1 KKWLQLKK 9

RESULT 4
US-09-881-490-162
; Sequence 162, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.331"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetylated
; /note= "Position 1 is acetylated"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-09-881-490-162

Query Match      100.0%; Score 48; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. NO. 5.4e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKWLQLKK 9
Db      1 KKWLQLKK 9

RESULT 5
US-09-881-490-164
; Sequence 164, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.333"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= D-Lys
/note= "Position 1 is D-Lysine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
/note= "The C-Terminus is Amidated"
SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-09-881-490-164
Query Match 100.0%; Score 48; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9
RESULT 6
US-09-881-490-173
Sequence 173, Application US/09881490
Patent No. US20020077298A:
GENERAL INFORMATION:
APPLICANT: Little II, Roger G.
Lim, Edward
Fadem, Mitchell B.
TITLE OF INVENTION: Anti-Fungal Peptides
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th FloorDrive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/881,490
FILING DATE: 14-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/119,858
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/372,105
FILING DATE: 13-JAN-95
APPLICATION NUMBER: 08/306,473
FILING DATE: 15-SEP-94
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-94
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-94
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-94

APPLICATION NUMBER: 08/093,202
FILING DATE: 15-JUL-93
APPLICATION NUMBER: 08/030,644
FILING DATE: 12-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 100-238/11021US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.342"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1, 2, 8 & 9
OTHER INFORMATION: /label= D-Lys
/note= "Positions 1, 2, 8 & 9 are D-lysine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
/note= "The C-Terminus is Amidated"
SEQUENCE DESCRIPTION: SEQ ID NO: 173:
US-09-881-490-173
Query Match 100.0%; Score 48; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKWLQLKK 9
Db 1 KKWLQLKK 9
RESULT 7
US-09-765-527-204
Sequence 204, Application US/09765527
Patent No. US20020006638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447


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;
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 204:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.348"
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-terminus
; OTHER INFORMATION: /label= Amidation
; /note- "The C-terminus is Amidated."
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 204:
US-09-765-527-204

Query Match 100.0%; Score 48; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKWLQLKK 9
Db 2 KKWLQLKK 10

RESULT 8
US-09-765-527-205
; Sequence 205, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
;
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
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; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.349"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-terminus
; OTHER INFORMATION: /label= Amidation
; /note- "The C-terminus is Amidated."
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 205:
US-09-765-527-205

Query Match 100.0%; Score 48; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 9
US-09-881-490-179
; Sequence 179, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 179:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
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;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: misc_feature
;; OTHER INFORMATION: "XMP.348"
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: C-Terminus
;; OTHER INFORMATION: /label= Amidation
;; /note= "The C-Terminus is Amidated"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 175:
US-09-881-490-179

Query Match 100.0%; Score 48; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKWLQLKK 9
Db 2 KKWLQLKK 10

RESULT 10

US-09-881-490-180
; Sequence 180, Application US/09881490
; Patent No. US2002007298A1

GENERAL INFORMATION:

APPLICANT: Little II, Roger G.

Lim, Edward

Fadem, Mitchell H.

TITLE OF INVENTION: Anti-Fungal Peptides

NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th FloorDrive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/881,490

FILING DATE: 14-Jun-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/119,858

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/372,105

FILING DATE: 13-JAN-95

APPLICATION NUMBER: 08/306,473

FILING DATE: 15-SEP-94

APPLICATION NUMBER: 08/273,540

FILING DATE: 11-JUL-94

APPLICATION NUMBER: 08/209,762

FILING DATE: 11-MAR-94

APPLICATION NUMBER: 08/183,222

FILING DATE: 14-JAN-94

APPLICATION NUMBER: 08/093,202

FILING DATE: 15-JUL-93

APPLICATION NUMBER: 08/030,644

FILING DATE: 12-MAR-93

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 100-238/11021US01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 180:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: misc_feature
;; OTHER INFORMATION: "XMP.349"
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: C-Terminus
;; OTHER INFORMATION: /label= Amidation
;; /note= "The C-Terminus is Amidated"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 180:
US-09-881-490-180

Query Match 100.0%; Score 48; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKWLQLKK 9
Db 1 KKWLQLKK 9

RESULT 11

US-09-765-527-206

; Sequence 206, Application US/097655527

; Patent No. US20020006638A1

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

TITLE OF INVENTION: Methods for Recombinant Microbial Production of
Fusion Proteins and BPI-Derived Peptides

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/765,527

FILING DATE: 18-Jan-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/621,803

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.

REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27129/33199

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 206:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: "XMP.350"

FEATURE:

NAME/KEY: Modified-site

LOCATION: C-Terminus

OTHER INFORMATION: /label= Amidation

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;
; /note= "The C-Terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 206;
US-09-765-527-206

Query Match      100.0%; Score 48; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKWLQLKK 9
Db      2 KKWLQLKK 10

RESULT 12
US-09-881-490-181
; Sequence 181, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little I., Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th Floor Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.350"
; FEATURE:

;
; /note= "The C-Terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 206;
US-09-765-527-206

Query Match      100.0%; Score 48; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKWLQLKK 9
Db      2 KKWLQLKK 10

RESULT 13
US-09-765-527-192
; Sequence 192, Application US/09765527
; Patent No. US2002006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 192:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.326"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 192;
US-09-765-527-192

Query Match      89.6%; Score 43; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKWLQLKK 8
```

Db 1 KWLIIQLK 8

RESULT 14

US-09-881-490-157

; Sequence 157, Application US/09881490

; Patent No. US20020077298A1

GENERAL INFORMATION:

APPLICANT: Little II, Roger G.

Lim, Edward

Fadem, Mitchell B.

TITLE OF INVENTION: Anti-Fungal Peptides

NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th FloorDrive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/881,490

FILING DATE: 14-Jun-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/119,858

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/372,105

FILING DATE: 13-JAN-95

APPLICATION NUMBER: 08/306,473

FILING DATE: 15-SEP-94

APPLICATION NUMBER: 08/273,540

FILING DATE: 11-JUL-94

APPLICATION NUMBER: 08/209,762

FILING DATE: 11-MAR-94

APPLICATION NUMBER: 08/183,222

FILING DATE: 14-JAN-94

APPLICATION NUMBER: 08/093,202

FILING DATE: 15-JUL-93

APPLICATION NUMBER: 08/030,644

FILING DATE: 12-MAR-93

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 100-238/11021US01

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 157:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: "XMP.324"

FEATURE:

NAME/KEY: Modified-site

LOCATION: C-Terminus

OTHER INFORMATION: /label= Amidation

/note= "The C-Terminus is Amidated"

SEQUENCE DESCRIPTION: SEQ ID NO: 157:

US-09-881-490-157

Query Match 89.6%; Score 43; DB 9; Length 8;

Best Local Similarity 100.0%; Pred. No. 5.4e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 KWLIIQLK 9

Db 1 KWLIIQLK 8

RESULT 15

US-09-881-490-159

; Sequence 159, Application US/09881490

; Patent No. US20020077298A1

GENERAL INFORMATION:

APPLICANT: Little II, Roger G.

Lim, Edward

Fadem, Mitchell B.

TITLE OF INVENTION: Anti-Fungal Peptides

NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th FloorDrive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/881,490

FILING DATE: 14-Jun-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/119,858

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/372,105

FILING DATE: 13-JAN-95

APPLICATION NUMBER: 08/306,473

FILING DATE: 15-SEP-94

APPLICATION NUMBER: 08/273,540

FILING DATE: 11-JUL-94

APPLICATION NUMBER: 08/209,762

FILING DATE: 11-MAR-94

APPLICATION NUMBER: 08/183,222

FILING DATE: 14-JAN-94

APPLICATION NUMBER: 08/093,202

FILING DATE: 15-JUL-93

APPLICATION NUMBER: 08/030,644

FILING DATE: 12-MAR-93

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 100-238/11021US01

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 159:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: "XMP.326"

FEATURE:

NAME/KEY: Modified-site

LOCATION: C-Terminus

OTHER INFORMATION: /label= Amidation

/note= "The C-Terminus is Amidated"

SEQUENCE DESCRIPTION: SEQ ID NO: 159:

US-09-881-490-159

Query Match 89.6%; Score 43; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKWLIQLK 8
| | | | | | | |
Db 1 KKWLIQLK 8

Search completed: October 14, 2003, 14:44:51
Job time : 21.9375 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 ; Search time 11.8125 Seconds
(without alignments)
73.271 Million cell updates/sec

Title: US-09-881-490-164
Perfect score: 48
Sequence: 1 KKWLQLKK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 37 | 77.1 | 189 | 2 AH1029 | probable membrane |
| 2 | 37 | 77.1 | 212 | 2 T31058 | hypothetical prote |
| 3 | 37 | 77.1 | 275 | 2 H81074 | phytoene synthase- |
| 4 | 36 | 75.0 | 70 | 2 G64500 | hypothetical prote |
| 5 | 36 | 75.0 | 89 | 2 F91003 | Kil protein (impor |
| 6 | 36 | 75.0 | 578 | 2 B71431 | hypothetical prote |
| 7 | 35 | 72.9 | 198 | 2 T51962 | Rac-like GTP bindi |
| 8 | 35 | 72.9 | 585 | 2 C70341 | acetolactate synth |
| 9 | 35 | 72.9 | 731 | 2 A99106 | hypothetical prote |
| 10 | 35 | 72.9 | 2655 | 2 D96595 | probable acetyl-Co |
| 11 | 34 | 70.8 | 59 | 2 AE2023 | hypothetical prote |
| 12 | 34 | 70.8 | 89 | 2 B85638 | probable Kil prote |
| 13 | 34 | 70.8 | 89 | 2 C85848 | hypothetical prote |
| 14 | 34 | 70.8 | 180 | 2 T37857 | hypothetical prote |
| 15 | 34 | 70.8 | 210 | 2 B40203 | 4-alpha-glucanotra |
| 16 | 34 | 70.8 | 276 | 2 D81868 | probable transfera |
| 17 | 34 | 70.8 | 285 | 2 A69748 | hypothetical prote |
| 18 | 34 | 70.8 | 287 | 2 B90540 | conserved hypothet |
| 19 | 34 | 70.8 | 382 | 2 S55166 | hypothetical prote |
| 20 | 34 | 70.8 | 547 | 2 A64991 | hypothetical ABC t |
| 21 | 34 | 70.8 | 547 | 2 D91016 | hypothetical prote |
| 22 | 34 | 70.8 | 547 | 2 F85860 | hypothetical prote |
| 23 | 34 | 70.8 | 4588 | 2 T28667 | dynein beta heavy |
| 24 | 34 | 70.8 | 4639 | 1 A54794 | dynein heavy chain |
| 25 | 34 | 70.8 | 4725 | 1 A44357 | dynein heavy chain |
| 26 | 33 | 68.8 | 53 | 2 S72388 | pd53 protein - Ent |
| 27 | 33 | 68.8 | 95 | 2 I39575 | nickel-cobalt-cadm |
| 28 | 33 | 68.8 | 185 | 2 D82418 | MutT/nudix family |
| 29 | 33 | 68.8 | 185 | 2 A96989 | transcription regu |

| | | | | | |
|----|----|------|-----|----------|--------------------|
| 30 | 33 | 68.8 | 201 | 2 T48862 | rac-like protein A |
| 31 | 33 | 68.8 | 209 | 2 T05164 | hypothetical prote |
| 32 | 33 | 68.8 | 220 | 2 AB0084 | probable DedA-fami |
| 33 | 33 | 68.8 | 233 | 2 D96763 | hypothetical prote |
| 34 | 33 | 68.8 | 252 | 2 F97072 | ABC transporter, A |
| 35 | 33 | 68.8 | 264 | 2 AE2787 | exopolysaccharide |
| 36 | 33 | 68.8 | 264 | 2 G97566 | exopolysaccharide |
| 37 | 33 | 68.8 | 335 | 2 A89834 | teichoic acid bios |
| 38 | 33 | 68.8 | 344 | 2 S46871 | Bl3R protein - var |
| 39 | 33 | 68.8 | 344 | 2 E72173 | D2R protein - vari |
| 40 | 33 | 68.8 | 344 | 2 T28611 | hypothetical prote |
| 41 | 33 | 68.8 | 367 | 2 AD3631 | nitrous-oxide redu |
| 42 | 33 | 68.8 | 396 | 2 T46901 | hypothetical prote |
| 43 | 33 | 68.8 | 585 | 2 A39286 | parathyroid hormon |
| 44 | 33 | 68.8 | 589 | 2 I59297 | parathyroid hormon |
| 45 | 33 | 68.8 | 591 | 2 S44203 | parathyroid hormon |

ALIGNMENTS

RESULT 1

AH1029
probable membrane protein STY4561 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AH1029
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Chur
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Fa
r, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH1029
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD09337.i; PID:gl6505337; GSPDB:GN00176
C:Genetics:
A:Gene: STY4561

Query Match 77.1%; Score 37; DB 2; Length 189;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9

Db 101 KRWLIQAKR 109

RESULT 2

T31058
hypothetical protein C05D9.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 17-Mar-2000
C:Accession: T31058
R:Fulton, L.; Gattung, S.
submitted to the EMBL Data Library, September 1999
A:Description: The sequence of C. elegans cosmid C05D9.
A:Reference number: 220960
A:Accession: T31058
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-212 <FUL>
A:Cross-references: EMBL:U64605; PIDN:AAB04584.1
A:Experimental source: strain Bristol N2
C:Genetics:
A:Map position: X
A:Introns: 21/3; 82/1; 161/2
A:Note: C05D9.5
C:Superfamily: translation initiation factor eIF-4E

Query Match 77.1% Score 37; DB 2; Length 212;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KWLIIQLKK 9
|||:||||
Db 110 KWLIIQLKK 117

RESULT 3
H81074
phytoene synthase-related protein NMB1521 [imported] - Neisseria meningitidis (strain MC58)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: H81074
R:Tettelin, H.; Saunders, N.J.; Heideberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, C.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.; Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Venter, A.; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755; PMID:10710307
A:Accession: H81074
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <NT>
A:Cross-references: GB:AE002501; GB:AE002098; NID:q7226755; PIDN:AAF41877.1; PID:q7226766
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1521

Query Match 77.1% Score 37; DB 2; Length 275;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KWLIIQLKK 9
| ||| |||
Db 263 KWLIIQLKK 271

RESULT 4
G64500
hypothetical protein MJ1608 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: G64500
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbook, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Rison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: G64500
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-70 <BUL>
A:Cross-references: GB:U67601; GB:L77117; NID:q2826439; PIDN:AAB99635.1; PID:g1500506; T51962
C:Genetics:
A:Map position: FOR1582918-1583130

Query Match 75.0% Score 36; DB 2; Length 70;
Best Local Similarity 75.0%; Pred. No. 7.4;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KWLIIQLKK 9
|||:||||
Db 63 KWLIIQLKK 70

RESULT 5
F91003

kil protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C:Accession: F91003
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.; DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F91003
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-89 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA36421.1; PID:g13362467; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECS2998
C:Superfamily: phage lambda kil protein

Query Match 75.0% Score 36; DB 2; Length 89;
Best Local Similarity 55.6%; Pred. No. 9.3;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KWLIIQLKK 9
|||:||||
Db 74 KWLIIQLKK 82

RESULT 6
B71431
hypothetical protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
A:Variety: Columbia
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998
C:Accession: B71431
R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; vanagagh, T.; Hempel, S.; Kottler, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, Nature 391, 485-488, 1998
A:Authors: Mueller-Auer, S.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; C.; Chalwatzis, N.
A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis A:Reference number: A71400; MUID:98121113; PMID:9461215
A:Accession: B71431
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-578 <BRV>
A:Cross-references: GB:Z97341; NID:g2244991; PID:e3266992; PID:g22445000
C:Genetics:
A:Map position: 4COP9-4G3845

Query Match 75.0% Score 36; DB 2; Length 578;
Best Local Similarity 87.5%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KWLIIQLKK 9
|||:||||
Db 30 KWLIIQLKK 37

RESULT 7
T51962
Rac-like GTP binding protein [imported] - Picea mariana
C:Species: Picea mariana
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-2000
C:Accession: T51962
R:Perry, D.J.; Bousquet, J.; Genetics 149, 1089-1098, 1998
A:Title: Sequence-tagged-site (STS) markers of arbitrary genes. Development, charact A:Reference number: 225268; MUID:98278823; PMID:9611216
A:Accession: T51962
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-198 <PEK>
A:Cross-references: EMBL:AF051223; PIDN:AAC32124.1
C:Genetics:
A:Note: Sb30
C:Superfamily: ras transforming protein; translation elongation factor Tu homology

Query Match 72.9%; Score 35; DB 2; Length 198;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLKK 8
| | | | |
Db 98 KKWLLELR 105

RESULT 8
C70341
acetylactate synthase (EC 4.1.3.18) large chain - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 15-Oct-1999
C:Accession: C70341
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: C70341
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-585 <AQF>
A:Cross-references: GH:AE000690; NID:g2983100; PIDN:AAC06706.1; PID:g2983101; GB:AE00069
A:Experimental source: strain VF5
C:Genetics:
A:Gene: ilvB
C:Superfamily: acetylactate synthase large chain; thiamin pyrophosphate-binding domain h
C:Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein; m
F:440-488/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 72.9%; Score 35; DB 2; Length 585;
Best Local Similarity 66.7%; Pred. No. 93;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
| | | | |
Db 351 KKWLEQIEK 359

RESULT 9
A99106
hypothetical protein orf731 [imported] - Guillardia theta nucleomorph
C:Species: nucleomorph Guillardia theta
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: A99106
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reil
Nature 410, 1091-1096, 2001
A:Title: The highly reduced genome of an ensiaved algal nucleus.
A:Reference number: A99082; MUID:11323671; PMID:11323671
A:Accession: A99106
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-731 <DOU>
A:Cross-references: GB:AJ010592; NID:g12580677; PIDN:CAC26995.1; GSPDB:GN00151
C:Genetics:
A:Gene: orf731
A:Map position: 2
A:Genome: nucleomorph
C:Keywords: nucleomorph

Query Match 72.9%; Score 35; DB 2; Length 731;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
| | | | |
Db 273 KKWIFLLKK 281

RESULT 10
D96595
probable acetyl-CoA synthetase, 45051-31547 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96595
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Al
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kir
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marz
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tal
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D96595
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2655 <STO>
A:Cross-references: GB:AE005173; NID:g10645429; PIDN:AAG21546.1; GSPDB:GN00141
C:Genetics:
A:Gene: F7A10.14
A:Map position: 1

Query Match 72.9%; Score 35; DB 2; Length 2655;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
| | | | |
Db 2335 KKWPIQLRR 2343

RESULT 11
AE2023
hypothetical protein asl1739 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AE2023
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iri
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Taba
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacteriu
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2023
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-59 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA073438.1; PID:g17130829; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: asl1739

Query Match 70.8%; Score 34; DB 2; Length 59;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
| | | | |
Db 47 KAWLVKLR 55

RESULT 12
B85638

probable kil protein of bacteriophage BP-933W kilw [imported] - Escherichia coli (strain C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C:Accession: B85638
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: B85638
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-89 <STO>
A:Cross-references: GB:AE005174; NID:gl2514292; PIDN:AAG55566.1; GSPDB:GN00145; UWGP:Z14
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
C:Superfamily: phage lambda kil protein
Query Match 70.8%; Score 34; DB 2; Length 89;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KKWLIOQLK 8
DB 74 KKWLMLK 81
RESULT 13
C85848
hypothetical protein Z3364 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C:Accession: C85848
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: C85848
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-89 <STO>
A:Cross-references: GB:AE005174; NID:gl2516417; PIDN:AAG57247.1; GSPDB:GN00145; UWGP:Z33
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
C:Superfamily: phage lambda kil protein
Query Match 70.8%; Score 34; DB 2; Length 89;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KKWLIOQLK 8
DB 74 KKWLMLK 81
RESULT 14
T37857
hypothetical protein SPAC17G8.05 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T37857
R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A:Reference number: Z21750
A:Accession: T37857
A:Status: preliminary; translated from GB/EMBL/CDBJ
A:Molecule type: DNA
A:Residues: 1-180 <DEV>
A:Cross-references: EMBL:Z69795; PIDN:CAA93698.1; GSPDB:GN00066; SPDB:SPAC17G8.05
A:Experimental source: strain 972h-; cosmid cl7G8

C:Genetics:
A:Gene: SPDB:SPAC17G8.05
A:Map position: 1
A:Introns: 22/1
Query Match 70.8%; Score 34; DB 2; Length 180;
Best Local Similarity 62.5%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KKWLIOQLK 8
DB 22 KKWVVOYK 29
RESULT 15
B40203
4-alpha-glucanotransferase (EC 2.4.1.25) / amylo-1,6-glucosidase (EC 3.2.1.33) - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 16-Aug-2002
C:Accession: B40203
R:Yang, B.Z.; Ding, J.H.; Enghild, J.J.; Bao, Y.; Chen, Y.T.
J. Biol. Chem. 267, 9294-9299, 1992
A:Title: Molecular cloning and nucleotide sequence of cDNA encoding human muscle gly
A:Reference number: A40203; MUID:92250533; PMID:1374391
A:Accession: B40203
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-210 <YAN>
C:Superfamily: 4-alpha-glucanotransferase / amylo-1,6-glucosidase
C:Keywords: glycosidase; glycosyltransferase; hexosyltransferase; hydrolase; polysac
Query Match 70.8%; Score 34; DB 2; Length 210;
Best Local Similarity 62.5%; Pred. No. 52;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 KWLIOQLK 9
DB 203 KWLELOK 210
Search completed: October 14, 2003, 14:38:06
Job time : 11.8125 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 ; Search time 6.375 Seconds
(without alignments)
66.391 Million cell updates/sec

Title: US-09-881-490-164
Perfect score: 48
Sequence: 1 KKWLIQLKK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 37 | 77.1 | 212 | 1 IFE4_CAEEL | Q22888 caenorhabdi |
| 2 | 36 | 75.0 | 70 | 1 YG08_METCA | Q59003 methanococc |
| 3 | 34 | 70.8 | 180 | 1 YD65_SCHPC | Q10317 schizosacch |
| 4 | 34 | 70.8 | 245 | 1 IFE3_HUMAN | Q60573 h eukaryoti |
| 5 | 34 | 70.8 | 245 | 1 IFE3_MOUSE | Q8bmb3 mus musculu |
| 6 | 34 | 70.8 | 382 | 1 YJ07_YEAST | P47007 saccharomyc |
| 7 | 34 | 70.8 | 430 | 1 SECY_STAAJ | O08387 staphylococ |
| 8 | 34 | 70.8 | 547 | 1 YGJL_FCOLI | P33941 escherichia |
| 9 | 34 | 70.8 | 4639 | 1 DYHC_DROME | P37276 drosophila |
| 10 | 34 | 70.8 | 4725 | 1 DYHC_DICDI | P34036 dictyoste.i |
| 11 | 33 | 68.8 | 95 | 1 NCCY_ALCXX | Q44581 alcaligenes |
| 12 | 33 | 68.8 | 201 | 1 RAC2_ARATH | Q38903 arabidopsis |
| 13 | 33 | 68.8 | 209 | 1 V282_ARATH | O6542: arabidopsis |
| 14 | 33 | 68.8 | 218 | 1 GCH1_PASMU | P57865 pasteurella |
| 15 | 33 | 68.8 | 267 | 1 EXOR_RHILV | Q52822 rhizobium l |
| 16 | 33 | 68.8 | 344 | 1 SPI2_VARV | P33830 variola vir |
| 17 | 33 | 68.8 | 396 | 1 PTD4_HUMAN | Q9n1k5 homo sapien |
| 18 | 33 | 68.8 | 396 | 1 PTD4_MOUSE | Q9cz30 mus musculu |
| 19 | 33 | 68.8 | 585 | 1 PTRR_DIDMA | P25107 didelphis m |
| 20 | 33 | 68.8 | 585 | 1 PTRR_PIG | P50133 sus scrofa |
| 21 | 33 | 68.8 | 591 | 1 PTRR_MOUSE | P41593 mus musculu |
| 22 | 33 | 68.8 | 591 | 1 PTRR_RAT | P25961 rattus norv |
| 23 | 33 | 68.8 | 593 | 1 PTRR_HUMAN | Q03431 homo sapien |
| 24 | 33 | 68.8 | 639 | 1 NOS2_RHIME | Q59746 rhizobium m |
| 25 | 33 | 68.8 | 650 | 1 MI10_CAEEL | P34400 caenorhabdi |
| 26 | 33 | 68.8 | 1742 | 1 MY5C_HUMAN | Q9nqx4 homo sapien |
| 27 | 33 | 68.8 | 1877 | 1 PKK5_MOUSE | Q04592 mus musculu |
| 28 | 33 | 68.8 | 2109 | 1 RRPL_VSVJH | P13615 vesicular s |
| 29 | 32 | 66.7 | 290 | 1 Y084_MYCGE | P47330 mycoplasma |
| 30 | 32 | 66.7 | 387 | 1 BODG_MOUSE | Q924y0 mus musculu |
| 31 | 32 | 66.7 | 387 | 1 BODG_RAT | Q9qzu7 rattus norv |
| 32 | 32 | 66.7 | 423 | 1 AATM_CHICK | P00508 gallus gall |
| 33 | 32 | 66.7 | 454 | 1 Y095_MYCPN | P75538 mycoplasma |

| | | | | | |
|----|------|------|------|--------------|--------------------|
| 34 | 32 | 66.7 | 470 | 1 MRS2_YEAST | Q01926 saccharomyc |
| 35 | 32 | 66.7 | 538 | 1 TH1P_HAFIN | P44985 haemophilus |
| 36 | 32 | 66.7 | 1067 | 1 CARB_CLOPE | Q8xhb3 clostridium |
| 37 | 32 | 66.7 | 1328 | 1 POLX_TOBAC | P10978 nicotiana t |
| 38 | 31.5 | 65.6 | 1953 | 1 BN11_YEAST | P41832 saccharomyc |
| 39 | 31 | 64.6 | 89 | 1 VKIL_LAMBD | P03758 bacterioph |
| 40 | 31 | 64.6 | 113 | 1 YB51_METJA | Q58551 methanococc |
| 41 | 31 | 64.6 | 124 | 1 LBD9_ARATH | O82198 arabidopsis |
| 42 | 31 | 64.6 | 152 | 1 FGF1_PIG | P20002 sus scrofa |
| 43 | 31 | 64.6 | 155 | 1 FGF1_CHICK | P19596 gallus gall |
| 44 | 31 | 64.6 | 155 | 1 FGF1_HUMAN | P05230 homo sapien |
| 45 | 31 | 64.6 | 155 | 1 FGF1_MESAU | P34004 mesocricetu |

ALIGNMENTS

RESULT 1
IFE4_CAEEL
ID IFE4_CAEEL STANDARD: PRT; 212 AA.
AC Q22888;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Eukaryotic translation initiation factor 4E (eIF-4E) (mRNA
cap-binding protein) (eIF-4F 25 kDa subunit).
GN IFE-4 OR C05D9.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=20209441; PubMed=10744754;
RA Kciper B.D., Lamphear B.J., Deshpande A.M., Jankowska-Anyszka M.,
RA Aamodt E.J., Blumenthal T., Rhoads R.E.;
RT "Functional characterization of five eIF4E isoforms in Caenorhabditis
elegans.";
RL J. Biol. Chem. 275:10590-10596(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Fulton L., Gattung S.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECOGNIZES AND BINDS THE 7-METHYLGUANOSINE-CONTAINING
MRNA "CAP" DURING AN EARLY STEP IN THE INITIATION OF PROTEIN
SYNTHESIS AND FACILITATES RIBOSOME BINDING BY INDUCING THE
UNWINDING OF THE MRNAS SECONDARY STRUCTURES.
CC -!- SUBUNIT: EIF4F IS A TRIMER COMPOSED OF EIF4E, EIF4G AND EIF4A
(WHICH CAN CYCLE IN AND OUT OF THE COMPLEX).
CC -!- SIMILARITY: BELONGS TO THE EUKARYOTIC INITIATION FACTOR 4E FAMILY.

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EMBL; AF214651; AAF62414.1; -.
EMBL; U64605; AAF98601.1; -.
PIR; T31058; T31058.
HSSP; P07260; 1AP8.
DR WormPep; C05D9.5; CE07931.
DR InterPro; IPR001040; TIF_eif_4E.
DR Pfam; PF01652; IF4E; 1.
DR ProDom; PD003697; TIF_eif_4E; 1.
DR PROSITE; PS00813; IF4E; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding;
KW Multigene family.
SQ SEQUENCE 212 AA; 24584 MW; 87BA3DFE9FE8A486 CRC64;


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Query Match          77.1%; Score 37; DB 1; Length 212;
Best Local Similarity 75.0%; Pred. No. 5.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 KWLIIQLK 9
DB 110 KWIIRLKK 17

RESULT 2
YD65_SCHPO STANDARD; PRI: 70 AA.
AC Q10317;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C17G8.05 in chromosome 1.
GN SPAC17G8.05.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

Query Match          75.0%; Score 36; DB 1; Length 70;
Best Local Similarity 75.0%; Pred. No. 2.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KWLIIQLK 8
DB 63 KKWVVKLK 70

RESULT 3
YD65_SCHPO STANDARD; PRI: 180 AA.
AC Q10317;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C17G8.05 in chromosome 1.
GN SPAC17G8.05.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

Query Match          77.1%; Score 37; DB 1; Length 212;
Best Local Similarity 75.0%; Pred. No. 5.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 KWLIIQLK 9
DB 110 KWIIRLKK 17

RESULT 2
YD65_SCHPO STANDARD; PRI: 70 AA.
AC Q10317;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C17G8.05 in chromosome 1.
GN SPAC17G8.05.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

Query Match          77.1%; Score 37; DB 1; Length 212;
Best Local Similarity 75.0%; Pred. No. 5.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 KWLIIQLK 9
DB 110 KWIIRLKK 17

RESULT 2
YD65_SCHPO STANDARD; PRI: 70 AA.
AC Q10317;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C17G8.05 in chromosome 1.
GN SPAC17G8.05.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
```

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OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckie E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT *The genome sequence of Schizosaccharomyces pombe.*;
RI Nature 415:871-880(2002).
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CC -----
CC EMBL: Z69795; CAA93688.1; -.
DR PIR: T37857; T37857.
DR GeneDB_SPombe; SPAC17G8.05; -.
KW Hypothetical protein.
SQ SEQUENCE 180 AA; 20931 MW; A471D5243297E0B2 CRC64;

Query Match          70.8%; Score 34; DB 1; Length 180;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KWLIIQLK 8
DB 22 KKWVVQYK 29

RESULT 4
IFE3_HUMAN STANDARD; PRI: 245 AA.
AC O60573; O75349;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Eukaryotic translation initiation factor 4E type 3 (eIF-4E type 3)
DE (eIF4E type 3) (mRNA cap-binding protein type 3) (Eukaryotic
DE translation initiation factor 4E-like 3) (Eukaryotic translation
DE initiation factor 4E homologous protein) (mRNA cap-binding protein
DE 4EHP) (eIF4E-like protein 4E-LP).
GN EIF4EL3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., CHARACTERIZATION, 3D-STRUCTURE MODELING, AND
RP MUTAGENESIS.
RC TISSUE=Follicle;
RX MEDLINE=98250763; PubMed=9562349;
RA Rom E., Kim H.C., Gingras A.-C., Marcotrigiano J., Favre D., Olsen H.,
RA Burley S.K., Sonenberg N.;
RT "Cloning and characterization of 4EHP, a novel mammalian eIF4E-related
RT cap-binding protein.";
RL J. Biol. Chem. 273:13104-13109(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Joshi B., Norris K.K., Jagus R.;
RT "Isolation of human and mouse cDNAs encoding novel eIF4E-like
RT proteins.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=98318631; PubMed=9653160;
RA Mao M., Fu G., Wu J.-S., Zhang Q.-H., Zhou J., Kan L.-X., Huang Q.-H.,
RA He K.-L., Gu B.-W., Han Z.-G., Shen Y., Gu J., Yu Y.-P., Xu S.-H.,
RA Wang Y.-X., Chen S.-J., Chen Z.;
RT "Identification of genes expressed in human CD34(+) hematopoietic
RT stem/progenitor cells by expressed sequence tags and efficient full-
RT length cDNA cloning.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8175-8180(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle, Urinary bladder, and Uterus;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huyle S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfield G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schcin J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Recognizes and binds the 7-methylguanosine-containing
CC mRNA "cap" during an early step in the initiation of protein
CC synthesis and facilitates ribosome binding by inducing the
CC unwinding of the mRNAs secondary structures.
CC -!- SUBUNIT: EIF4F is a trimer composed of EIF4E, EIF4G and EIF4A
CC (which can cycle in and out of the complex) (By similarity).
CC -!- SIMILARITY: BELONGS TO THE EUKARYOTIC INITIATION FACTOR 4E FAMILY.
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CC -----
DR EMBL; AF047695; AAC18565.1; -
DR EMBL; AF068117; AAC19374.1; -
DR EMBL; AF038957; AAC39871.1; -
DR EMBL; BC005392; AAH05392.1; -

DR EMBL; BC005874; AAH05874.1; -
DR EMBL; BC021226; AAH21226.1; -
DR EMBL; BC021690; AAH21690.1; -
DR Genew; HGNC:3293; EIF4EL3.
DR MIM; 605895; -
DR GO; GO:0003731; F:mrna cap binding; TAS.
DR GO; GO:0006445; P:regulation of translation; TAS.
DR InterPro; IPR001040; TIF_eIF_4E.
DR Pfam; PF01652; IF4E; 1.
DR ProDom; PD003697; TIF_eIF_4E; 1.
DR PROSITE; PS00813; IF4E; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding;
KW Multigene family.
FT MUTAGEN 63 63 W->A: UNABLE TO BIND CAPPED RNA.
FT MUTAGEN 95 95 W->A: ABILITY TO BIND CAPPED MRNA REDUCED
FT 124 126 TO 40% OF WILD-TYPE.
FT MUTAGEN 124 124 WED->FAA: UNABLE TO BIND CAPPED RNA.
FT MUTAGEN 124 124 W->A: ABILITY TO BIND CAPPED MRNA REDUCED
FT 124 124 TO LESS THAN 10% OF WILD-TYPE.
FT MUTAGEN 124 124 W->F: ABILITY TO BIND CAPPED MRNA REDUCED
FT 125 125 TO 13% OF WILD-TYPE.
FT MUTAGEN 125 125 E->A: ABILITY TO BIND CAPPED MRNA REDUCED
FT 126 126 TO LESS THAN 10% OF WILD-TYPE.
FT MUTAGEN 126 126 D->A: SLIGHT REDUCTION IN ABILITY TO BIND
FT 135 135 CAPPED RNA.
FT MUTAGEN 148 148 W->A: UNABLE TO BIND CAPPED RNA.
FT MUTAGEN 183 183 W->A: ABILITY TO BIND CAPPED MRNA REDUCED
FT 183 183 TO LESS THAN 10% OF WILD-TYPE.
FT MUTAGEN 183 183 W->F: UNABLE TO BIND CAPPED RNA.
FT CONFLICT 1 27 MNKFDALKDDSDGHDQNEENSTQKD -> MMTVGTGTMIRM
FT KKTAKRKI (IN REF. 3).
SQ SEQUENCE 245 AA; 28362 MW; 3D3075BFA48B3C12 CRC64;
Query Match 70.8%; Score 34; DB 1; Length 245;
Best Local Similarity 62.5%; Pred. NO. 22;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 KWLQLKK 9
DB 134 KWIIRLRK 141
RESULT 5
IFE3_MOUSE
ID IFE3_MOUSE STANDARD; PRT; 245 AA.
AC Q8BMB3; O88503;
DI 15-SEP-2003 (Rel. 42, Created)
DI 15-SEP-2003 (Rel. 42, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Eukaryotic translation initiation factor 4E type 3 (eIF-4E type 3)
DE (eIF4E type 3) (mRNA cap-binding protein type 3) (Eukaryotic
DE translation initiation factor 4E-like 3) (eIF4E-like protein 4E-LP).
GN EIF4EL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH Swiss;
RA Joshi B., Jagus R.;
RT "Isolation of human and mouse cDNAs encoding novel eIF4E-like
RT proteins.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Ienhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
CC -!- FUNCTION: Recognizes and binds the 7-methylguanosine-containing
CC mRNA "CAP" during an early step in the initiation of protein
CC synthesis and facilitates ribosome binding by inducing the
CC unwinding of the mRNA secondary structures (By similarity).
CC -!- SUBUNIT: EIF4F is a trimer composed of EIF4E, EIF4G and EIF4A
CC (which can cycle in and out of the complex) (By similarity).
CC -!- SIMILARITY: BELONGS TO THE EUKARYOTIC INITIATION FACTOR 4E FAMILY.
CC -----
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CC -----
CC EMBL; AF068116; AAC19373.1; -;
DR EMBL; AK032965; BAC28102.1; -;
DR MGD; MGI:1914440; Eif4el3.
DR InterPro; IPR001040; TIF_eIF_4E.
DR Pfam; PF01652; IF4E; 1.
DR ProDom; PD003697; TIF_eIF_4E; 1.
DR PROSITE; PS00813; IF4E; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding;
KW Multigene family.
FT CONFLICT 200 200 L -> F (IN REF. 1).
SQ SEQUENCE 245 AA; 28263 MW; AA722843721A01CC CRC64;

Query Match 70.8%; Score 34; DB 1; Length 245;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 KWLQLKK 9
Db 134 KWIIRLK 141
|:|:|:|

RESULT 6
YJ07_YEAST
ID YJ07_YEAST STANDARD; PRT; 382 AA.
AC P47007;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Hypothetical 44.9 kDa protein in INO1-IDS2 intergenic region.
GN YJL147C OR J0639.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=96408771; PubMed=8813765;
RA Katsoulou C., Tzermia M., Tavernarakis N., Alexandraki D.;
RT "Sequence analysis of a 40.7 kb segment from the left arm of yeast
RT chromosome X reveals 14 known genes and 13 new open reading frames
RT including homologues of genes clustered on the right arm of
RT chromosome XI";
RL Yeast 12:787-797(1996).
CC -----
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CC -----
CC EMBL; Z49422; CAA89442.1; -;
DR EMBL; X87371; CAA60808.1; -;
DR PIR; S55166; S55166.
DR SGD; S0003683; YJL147C.
KW Hypothetical protein.
SQ SEQUENCE 382 AA; 44862 MW; DDAAF588AF9A3234 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 382;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKWLIQLKK 9
Db 298 KKWLIDIVK 306
|:|:|:|:|

RESULT 7
SECY_STAAU
ID SECY_STAAU STANDARD; PRT; 430 AA.
AC O08387;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Preprotein translocase secY subunit.
GN SECY.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCITC 8325;
RA Segarra R.A., Iandolo J.J.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH SECA AND SECE
CC TO ALLOW THE TRANSLOCATION OF PROTEINS ACROSS THE PLASMA MEMBRANE,
CC BY FORMING PART OF A CHANNEL.
CC -!- SUBUNIT: ONE OF SEVEN SECRETORY PROTEINS (SECA-F & SECY) THAT
CC COMPRISE THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
CC -----
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CC -----
CC EMBL; U96620; AAB54022.1; -;
DR InterPro; IPR002208; SecY.
DR Pfam; PF00344; secY; 1.

DR PRINTS: PRO0303; SECYTRNLASE.
DR TIGRFAMS; TIGR00967; 3a0501s007; 1.
DR PROSITE; PS00755; SECY_1; 1.
DR PROSITE; PS00756; SECY_2; 1.
KW Protein transport; Translocation; Transmembrane.
SQ SEQUENCE 430 AA; 47612 MW; AF6923FE32434031 CMC64;

Query Match 70.8%; Score 34; DB 1; Length 430;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLK 8
DB 333 KKWLITL 340

RESULT 8
YOJL_ECOLI STANDARD; PRT; 547 AA.
AC P33941; P33942;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical ABC transporter ATP-binding protein yojI.
GN YOJL OR B2211.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / RHB2600;
RA Richterich P., Lakey N., Gryan G., Jaehn L., Minz L., Robison K.,
RA Church G.M.;
RL Submitted (OCI-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampei G., Seki Y., Sivasubram S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
(Probable).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. SIMILAR TO
CC P.SYRINGAE SYRD.
CC
CC
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CC
CC
CC EMBL; U00008; AAA16403.1; -.
CC EMBL; AE000310; AAC75271.1; -.

DR EMBL; D90850; BAA15994.1; -.
DR PIR; A64991; A64991.
DR EcoGene; EGI2070; yojI.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABC_TM_transporter.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR005898; Cyc_pep_transporter.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMS; TIGR01194; cyc_pep_transpr; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW Hypothetical protein; ATP-binding; Transport; Transmembrane;
KW Inner membrane; Complete proteome.
FT TRANSMEM 16 36 POTENTIAL.
FT TRANSMEM 48 68 POTENTIAL.
FT TRANSMEM 125 145 POTENTIAL.
FT TRANSMEM 149 169 POTENTIAL.
FT TRANSMEM 240 260 POTENTIAL.
FT TRANSMEM 270 290 POTENTIAL.
FT NP_BIND 356 363 ATP (POTENTIAL).
SQ SEQUENCE 547 AA; 61552 MW; 11523935EDFD9EAB CRC64;

Query Match 70.8%; Score 34; DB 1; Length 547;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLK 8
DB 426 EKWLAQLK 433

RESULT 9
DYHC_DROME STANDARD; PRT; 4639 AA.
ID DYHC_DROME
AC P37276;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dynein heavy chain, cytosolic (DYHC).
GN CDHC OR DHC64C.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94375524; PubMed=8089180;
RA Li M., McGrail M., Serr M., Hays T.S.;
RT "Drosophila cytoplasmic dynein, a microtubule motor that is
asymmetrically localized in the oocyte.";
RL J. Cell Biol. 126:1475-1494(1994).
RN [2]
RP SEQUENCE OF 1877-1998 FROM N.A.
RX MEDLINE=94243034; PubMed=8186464;
RA Rasmussen K., Serr M., Gepner J., Gibbons I., Hays T.S.;
RT "A family of dynein genes in Drosophila melanogaster.";
RL Mol. Biol. Cell 5:45-55(1994).
CC -!- FUNCTION: Cytoplasmic dynein acts as a motor for the intracellular
CC retrograde motility of vesicles and organelles along microtubules.
CC Dynein has ATPase activity; the force-producing power stroke is
CC thought to occur on release of ADP.
CC -!- SUBUNIT: Consists of at least two heavy chains and a number of
CC intermediate and light chains.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem
CC (which binds cargo and interacts with other dynein components),
CC and the head or motor domain. The motor contains six tandemly-
CC linked AAA domains in the head, which form a ring. A stalk-like
CC structure (formed by two of the coiled coil domains) protrudes

CC between AAA 4 and AAA 5 and terminates in a microtubule-binding
CC site. A seventh domain may also contribute to this ring; it is not
CC clear whether the N-terminus or the C-terminus forms this extra
CC domain. There are four well-conserved and two non-conserved ATPase
CC sites, one per AAA domain. Probably only one of these (within AAA
CC 1) actually hydrolyzes ATP, the others may serve a regulatory
CC function.
CC
CC -!- SIMILARITY: Belongs to the dynein heavy chain family.
CC
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CC
CC EMBL; L23195; AAA60323.1; -.
CC EMBL; L25122; AAA28492.1; -.
CC PIR; A54794; A54794.
CC FlyBase; FBgn0010349; Dhc64C.
CC GO; GO:0045169; C:fusome; NAS.
CC GO; GO:0008567; F:dynein ATPase activity; IDA.
CC GO; GO:0003777; F:microtubule motor activity; IDA.
CC GO; GO:0007098; P:centrosome cycle; IMP.
CC GO; GO:0045478; P:fusome organization and biogenesis; NAS.
CC GO; GO:0007018; P:microtubule-based movement; IDA.
CC GO; GO:0007294; P:oocyte determination; IMP.
CC GO; GO:0007292; P:oogenesis; IMP.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR004273; Dynein_heavy.
CC Pfam; PF03028; Dynein_heavy; 1.
CC SMART; SM00382; AAA; 4.
CC Motor protein; Dynein; Microtubules; ATP-binding; Repeat; Coiled coil.
KW DOMAIN 1 1856 STEM (BY SIMILARITY).
FT DOMAIN 1857 2084 AAA 1 (BY SIMILARITY).
FT DOMAIN 2166 2437 AAA 2 (BY SIMILARITY).
FT DOMAIN 2541 2790 AAA 3 (BY SIMILARITY).
FT DOMAIN 2884 3153 AAA 4 (BY SIMILARITY).
FT DOMAIN 3189 3478 STALK (BY SIMILARITY).
FT DOMAIN 3539 3768 AAA 5 (BY SIMILARITY).
FT DOMAIN 3989 4205 AAA 6 (BY SIMILARITY).
FT DOMAIN 530 565 COILED COIL (POTENTIAL).
FT DOMAIN 774 794 COILED COIL (POTENTIAL).
FT DOMAIN 1264 1368 COILED COIL (POTENTIAL).
FT DOMAIN 3189 3261 COILED COIL (POTENTIAL).
FT DOMAIN 3382 3478 COILED COIL (POTENTIAL).
FT DOMAIN 3723 3782 COILED COIL (POTENTIAL).
FT NP_BIND 1895 1902 ATP (POTENTIAL).
FT NP_BIND 2210 2217 ATP (POTENTIAL).
FT NP_BIND 2580 2587 ATP (POTENTIAL).
FT NP_BIND 2922 2929 ATP (POTENTIAL).
SQ SEQUENCE 4639 AA; 530152 MW; 057A7D8800CCD07E CRC64;

Query Match 70.8%; Score 34; DB 1; Length 4639;
Best Local Similarity 62.5%; Pred. No. 3.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 KWLQLKK 9
:|:|:|
Db 4088 QWLVLKK 4095

RESULT 10
DYHC_DICDI
ID DYHC_DICDI STANDARD; PRT; 4725 AA.
AC P34036;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dynein heavy chain, cytosolic (DYHC).
GN DHCA.
OS Dictyostelium discoideum (Slime mold).

OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX3;
RX MEDLINE=93107159; PubMed=1469051;
RA Koonce M.P., Grissom P.M., McIntosh J.R.;
RT "Dynein from Dictyostelium: Primary structure comparisons between a
RT cytoplasmic motor enzyme and flagellar dynein.";
RL J. Cell Biol. 119:1597-1604(1992).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=95170719; PubMed=7866389;
RA Koonce M.P., Grissom P.M., Lyon M., Pope T., McIntosh J.R.;
RT "Molecular characterization of a cytoplasmic dynein from
RT Dictyostelium.";
RL J. Eukaryot. Microbiol. 41:645-651(1994).
CC -!- FUNCTION: Cytoplasmic dynein acts as a motor for the intracellular
CC retrograde motility of vesicles and organelles along microtubules.
CC Dynein has ATPase activity; the force-producing power stroke is
CC thought to occur on release of ADP.
CC -!- SUBUNIT: Consists of at least two heavy chains and a number of
CC intermediate and light chains.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem
CC (which binds cargo and interacts with other dynein components),
CC and the head or motor domain. The motor contains six tandemly-
CC linked AAA domains in the head, which form a ring. A stalk-like
CC structure (formed by two of the coiled coil domains) protrudes
CC between AAA 4 and AAA 5 and terminates in a microtubule-binding
CC site. A seventh domain may also contribute to this ring; it is not
CC clear whether the N-terminus or the C-terminus forms this extra
CC domain. There are four well-conserved and two non-conserved ATPase
CC sites, one per AAA domain. Probably only one of these (within AAA
CC 1) actually hydrolyzes ATP, the others may serve a regulatory
CC function.
CC -!- SIMILARITY: Belongs to the dynein heavy chain family.
CC
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CC
CC EMBL; Z15124; CAA78827.1; -.
CC PIR; A44357; A44357.
CC DictyDb; DD01045; dhca.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR004273; Dynein_heavy.
CC Pfam; PF03028; Dynein_heavy; 1.
CC SMART; SM00382; AAA; 3.
KW Motor protein; Dynein; Microtubules; ATP-binding; Repeat; Coiled coil.
FT DOMAIN 1 1930 STEM (BY SIMILARITY).
FT DOMAIN 1931 2153 AAA 1 (BY SIMILARITY).
FT DOMAIN 2233 2526 AAA 2 (BY SIMILARITY).
FT DOMAIN 2630 2880 AAA 3 (BY SIMILARITY).
FT DOMAIN 2973 3247 AAA 4 (BY SIMILARITY).
FT DOMAIN 3266 3580 STALK (BY SIMILARITY).
FT DOMAIN 3633 3862 AAA 5 (BY SIMILARITY).
FT DOMAIN 4093 4307 AAA 6 (BY SIMILARITY).
FT DOMAIN 864 897 COILED COIL (POTENTIAL).
FT DOMAIN 1199 1219 COILED COIL (POTENTIAL).
FT DOMAIN 1338 1367 COILED COIL (POTENTIAL).
FT DOMAIN 1420 1436 COILED COIL (POTENTIAL).
FT DOMAIN 1656 1684 COILED COIL (POTENTIAL).
FT DOMAIN 2226 2248 COILED COIL (POTENTIAL).
FT DOMAIN 2437 2457 COILED COIL (POTENTIAL).
FT DOMAIN 3266 3344 COILED COIL (POTENTIAL).
FT DOMAIN 3478 3580 COILED COIL (POTENTIAL).
FT DOMAIN 3849 3876 COILED COIL (POTENTIAL).
FT NP_BIND 1969 1976 ATP (POTENTIAL).


```
FT NP_BIND 2271 2278 ATP (POTENTIAL).
FT NP_BIND 2669 2676 ATP (POTENTIAL).
FT NP_BIND 3011 3018 ATP (POTENTIAL).
SQ SEQUENCE 4725 AA; 538607 MW; 9A0319915D579D3A CRC64;

Query Match 70.8%; Score 34; DB 1; Length 4725;
Best Local Similarity 62.5%; Pred. No. 3.8e-02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KWLQLKK 9
Db 4190 QWLVOLEK 4197

RESULT 11
NCCY_ALCXX
ID NCCY_ALCXX STANDARD; PRT; 95 AA.
AC Q44581;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Nickel-cobalt-cadmium resistance protein nccy.
GN NCCY.
OS Alcaligenes xylosoxydans xylosoxydans (Achromobacter xylosoxydans).
OG plasmid pTOM9.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Achromobacter.
OX NCBI_TaxID=515;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=31A;
RX MEDLINE=95050278; PubMed=7961470;
RA Schmidt T., Schlegel H.G.;
RT "Combined nickel-cobalt-cadmium resistance encoded by the ncc locus
of Alcaligenes xylosoxydans 31A."
RL J. Bacteriol. 176:7045-7054(1994).
CC -!- FUNCTION: COMPONENT OF THE NCC CATION-EFFLUX SYSTEM THAT CONFERES
RESISTANCE TO NICKEL, COBALT AND CADMIUM. MAY BE INVOLVED IN THE
REGULATION OF NCC.
CC -!- SIMILARITY: TO A. EUTROPHUS CNKY.
CC -----
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CC -----
DR EMBL; L31363; AAA65101.1; -.
DR PIR; I39575; I39575.
KW Plasmid; Nickel; Cobalt; Cadmium.
SQ SEQUENCE 95 AA; 10422 MW; 4524AA1F3EB37987 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 95;
Best Local Similarity 62.5%; Pred. No. 14;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KWLQLKK 9
Db 6 EWLVOAKK 13

RESULT 12
RAC2_ARATH
ID RAC2_ARATH STANDARD; PRT; 201 AA.
AC Q38903;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RAC-like GTP binding protein ARAC2.
GN ARAC2 OR AT5G45970 OR MCL19.1.
OS Arabidopsis thaliana (Mouse-ear cress).
```

```
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=98009984; PubMed=9349271;
RA Winge P., Brembu T., Bones A.M.;
RT "Cloning and characterization of rac-like cDNAs from Arabidopsis
thaliana.";
RL Plant Mol. Biol. 35:483-495(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RA Winge P., Brembu T., Kristensen R., Bones A.M.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=98069011; PubMed=9405937;
RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.
Sequence features of the regions of 1,044,062 bp covered by thirteen
physically assigned pl clones.";
RL DNA Res. 4:291-300(1997).
CC -!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE ROOT, HYPOCOTYL
AND STEM.
CC -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
CC -----
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CC -----
DR EMBL; U43026; AAC49852.1; -.
DR EMBL; AF115469; AAF40241.1; -.
DR EMBL; AB006698; BAB08242.1; -.
DR PIR; T48862; T48862.
DR HSSP; P21181; 1AM4.
DR InterPro; IPR003578; GTPase_Rho.
DR InterPro; IPR001806; Ras_trnsfrmng.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00071; ras; 1.
DR PRINTS; PR00449; RASTRNSFRMNG.
DR SMART; SM00174; RHO; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
KW GTP-binding; Prenylation; Lipoprotein.
FT NP_BIND 13 20 GTP (BY SIMILARITY).
FT NP_BIND 60 64 GTP (BY SIMILARITY).
FT NP_BIND 118 121 GTP (BY SIMILARITY).
FT DOMAIN 35 43 EFFECTOR REGION (POTENTIAL).
FT LIPID 198 198 GERANYL-GERANYL (POTENTIAL).
SQ SEQUENCE 201 AA; 22393 MW; B3E73F55BDBB8028 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 201;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KWLQLKK 8
Db 98 KWLPELK 105

RESULT 13
V282_ARATH
ID V282_ARATH STANDARD; PRT; 209 AA.
AC O65421;
DT 16-OCT-2001 (Rel. 40, Created)
```

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE VPS28 protein homolog 2.
GN AT4G21560 OR F18E5.180 OR F17L22.20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Voickaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
RA Harris B., Ansoerge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delsen Y., Puigdomenech P., Watson M., Schmidheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Rautry M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voel M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenegger T., Bothe G., Kampsperger U., Hilbert H., Braun M.,
RA Holzner E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Moolijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Alien S.,
RA Clark L., Doggett J., Hall S., Kay M., Leonard N., McIlay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloeker H., Scharfe M., Grimm M., Joehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argirliou A., Vitale D., Liguori R., Piravandi E.,
RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chedford F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bieleke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Graco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:769-777(1999).
CC -!- SIMILARITY: BELONGS TO THE VPS28 FAMILY.

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CC EMBL; AL022603; CAA18720.1; -.
DR EMBL; AL035527; CAB36800.1; -.
DR EMBL; AL161555; CAB81263.1; -.
DR PIR; T05164; T05164.

DR Pfam: PF03997; VPS28; 1.
KW Hypothetical protein; Transport; Protein transport.
SQ SEQUENCE 209 AA; 23494 MW; 8A8BB4B415D9786B CRC64;

Query Match 68.8%; Score 33; DB 1; Length 209;
Best Local Similarity 55.6%; Pred. NO. 29;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
|:|:|:| |
DB 166 KEWLLRLSK 174

RESULT 14
GCHL_PASMU
ID GCHL_PASMU STANDARD; PRT; 218 AA.
AC P57865;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE GTP cyclohydrolase I (EC 3.5.4.16) (GTP-CH-I).
GN FOLE OR PM0693.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RA MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
KT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -!- CATALYTIC ACTIVITY: GTP + 2 H(2)O -> formate + 2-amino-4-hydroxy-6-
CC (erythro-1,2,3-trihydroxypropyl) dihydropteridine triphosphate.
CC -!- PATHWAY: Tetrahydrofolate biosynthesis; first step.
CC -!- SUBUNIT: Homopolymer (by similarity).
CC -!- SIMILARITY: BELONGS TO THE GTP CYCLOHYDROLASE I FAMILY.

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CC EMBL; AF006106; AAK02777.1; -.
DR HSSP; P27511; 1A8R.
DR HAMAP; MF_00223; -; 1.
DR InterPro; IPR001474; GTP_cyclohydrol.
DR Pfam; PF01227; GTP_cyclohydrol; 1.
DR ProDom; PD003330; GTP_cyclohydrol; 1.
DR TIGRFAMs; TIGR00063; fole; 1.
DR PROSITE; PS00859; GTP_CYCLOHYDROL_1_1; 1.
DR PROSITE; PS00860; GTP_CYCLOHYDROL_1_2; 1.
KW One-carbon metabolism; Hydrolase; Complete proteome.
FT DISULFID 109 180 BY SIMILARITY.
SQ SEQUENCE 218 AA; 24953 MW; 12F1FC8129E790C9 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. NO. 30;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKWLQLKK 9
|:|:|:| |
DB 127 KKWVGLSK 135

RESULT 15
EXOR_RHILV
ID EXOR_RHILV STANDARD; PRT; 267 AA.
AC Q52822;

DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Exopolysaccharide production negative regulator precursor.
GN EXOR.
OS Rhizobium leguminosarum (biovar viciae).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID-387;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WSM710 / WR6-35;
RX MEDLINE-97346048; PubMed-9202471;
RA Reeve W.G., Dilworth M.J., Tiwari R.P., Glenn A.R.;
RT "Regulation of exopolysaccharide production in Rhizobium leguminosarum
RT biovar viciae WSM710 involves exoR.";
RL Microbiology 143:1951-1958(1997).
CC -!- FUNCTION: NEGATIVELY MODULATES EXOPOLYSACCHARIDE (EPS)
CC BIOSYNTHESIS.
CC -----
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CC -----
DR EMBL; L39937; AAB63941.1; -.
DR InterPro; IPR006597; Sel_like.
DR SMART; SM00671; SEL; 3.
KW Exopolysaccharide synthesis; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 267 EXOPOLYSACCHARIDE PRODUCTION NEGATIVE
FT REGULATOR.
SQ SEQUENCE 267 AA; 28922 MW; E45E2E0538E1F573 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 267;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKWL1QLKK 9
 | | | | | : |
Db 185 KKWLNQARK 193

Search completed: October 14, 2003, 14:34:08
Job time : 6.54167 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 ; Search time 29.8125 Seconds
(without alignments)
77.903 Million cell updates/sec

Title: US-09-881-490-164
Perfect score: 48
Sequence: 1 KKWLJQLKK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 40 | 83.3 | 359 | 2 Q93CS6 | Q93CS6 shigella bo |
| 2 | 38 | 79.2 | 229 | 5 Q8MP31 | Q8MP31 dictyosceli |
| 3 | 37 | 77.1 | 199 | 16 Q8Z1K3 | Q8Z1K3 salmonella |
| 4 | 37 | 77.1 | 275 | 16 Q9JYL8 | Q9JYL8 neisseria m |
| 5 | 36 | 75.0 | 99 | 2 Q9EYA7 | Q9EYA7 escherichia |
| 6 | 36 | 75.0 | 278 | 4 Q9UJ05 | Q9UJ05 homo sapien |
| 7 | 36 | 75.0 | 284 | 4 Q96BV3 | Q96BV3 homo sapien |
| 8 | 36 | 75.0 | 459 | 10 Q8H3G5 | Q8H3G5 oryza sativ |
| 9 | 36 | 75.0 | 578 | 10 Q23488 | Q23488 arabidopsis |
| 10 | 36 | 75.0 | 652 | 5 Q8I427 | Q8I427 plasmodium |
| 11 | 36 | 75.0 | 1566 | 5 Q9N3E9 | Q9N3E9 caenorhabdi |
| 12 | 35 | 72.9 | 136 | 16 Q8EI76 | Q8EI76 shewanella |
| 13 | 35 | 72.9 | 198 | 10 Q65062 | Q65062 picea maria |
| 14 | 35 | 72.9 | 261 | 16 Q9CNC3 | Q9CNC3 pasteurella |
| 15 | 35 | 72.9 | 294 | 8 Q8HIS8 | Q8HIS8 monosiga br |
| 16 | 35 | 72.9 | 338 | 5 Q01679 | Q01679 bombyx mori |

| | | | | | |
|----|----|------|------|-----------|--------------------|
| 17 | 35 | 72.9 | 381 | 16 Q8DSD4 | Q8dsd4 streptococc |
| 18 | 35 | 72.9 | 585 | 16 Q66759 | Q66759 aquifex aeo |
| 19 | 35 | 72.9 | 643 | 5 Q8IIV6 | Q8iiv6 plasmodium |
| 20 | 35 | 72.9 | 731 | 10 Q9AW75 | Q9aw75 guillardia |
| 21 | 35 | 72.9 | 767 | 10 Q8GXD0 | Q8gxd0 arabidopsis |
| 22 | 35 | 72.9 | 2655 | 10 Q9C8A3 | Q9c8a3 arabidopsis |
| 23 | 34 | 70.8 | 59 | 16 Q8YVW7 | Q8yvw7 anabaena sp |
| 24 | 34 | 70.8 | 89 | 9 Q9XJ11 | Q9xj11 bacterioph |
| 25 | 34 | 70.8 | 89 | 16 Q8XE88 | Q8xeh8 escherichia |
| 26 | 34 | 70.8 | 115 | 16 Q8CV09 | Q8cv09 oceanobacil |
| 27 | 34 | 70.8 | 234 | 11 Q9D334 | Q9d334 mus musculu |
| 28 | 34 | 70.8 | 235 | 16 Q8XL88 | Q8xl88 clostridium |
| 29 | 34 | 70.8 | 245 | 4 Q60573 | Q60573 homo sapien |
| 30 | 34 | 70.8 | 245 | 11 Q88503 | Q88503 mus musculu |
| 31 | 34 | 70.8 | 245 | 11 Q8BMB3 | Q8bmb3 mus musculu |
| 32 | 34 | 70.8 | 276 | 16 Q9JTL7 | Q9jtl7 neisseria m |
| 33 | 34 | 70.8 | 285 | 16 Q31436 | Q31436 bacillus su |
| 34 | 34 | 70.8 | 287 | 16 Q98QY4 | Q98qy4 mycoplasma |
| 35 | 34 | 70.8 | 343 | 1 Q9HH38 | Q9hh38 methanobact |
| 36 | 34 | 70.8 | 432 | 2 Q8GCX1 | Q8gcx1 enterococcu |
| 37 | 34 | 70.8 | 521 | 5 Q9VPX7 | Q9vpvx7 drosophila |
| 38 | 34 | 70.8 | 526 | 4 Q9Y3N2 | Q9y3n2 homo sapien |
| 39 | 34 | 70.8 | 547 | 16 Q8XE44 | Q8xe44 escherichia |
| 40 | 34 | 70.8 | 547 | 16 Q8FFQ4 | Q8ffq4 escherichia |
| 41 | 34 | 70.8 | 732 | 16 Q99XP7 | Q99xp7 streptococc |
| 42 | 34 | 70.8 | 732 | 16 Q8K5K3 | Q8k5k3 streptococc |
| 43 | 34 | 70.8 | 839 | 5 Q961M8 | Q961m8 drosophila |
| 44 | 34 | 70.8 | 954 | 4 Q8WVX8 | Q8wxv8 homo sapien |
| 45 | 34 | 70.8 | 957 | 4 Q9H0V3 | Q9hov3 homo sapien |

ALIGNMENTS

RESULT 1

Q93CS6 PRELIMINARY; PRT; 369 AA.
ID Q93CS6
AC Q93CS6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative glycosyl transferase.
GN WBAT.
OS Shigella boydii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21481970; PubMed=11598067;
RA Wang L., Qu W., Reeves P.R.;
RT "Sequence Analysis of Four Shigella boydii O-Antigen Loci: Implication for Escherichia coli and Shigella Relationships.";
RL Infect. Immun. 69:6923-6930(2001).
DR EMBL; AF402314; AAL27338.1; .
DR InterPro; IPR001296; Glyco_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Transferase.
SQ SEQUENCE 369 AA; 42760 MW; 3E2CCE371A6BA0BB CRC64;

Query Match 83.3%; Score 40; DB 2; Length 369;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKWLJQLKK 9
|||||:
Db 359 KKWLJQLKK 367

RESULT 2

Q8MP31 PRELIMINARY; PRT; 229 AA.
ID Q8MP31
AC Q8MP31;

DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and Analysis of Chromosome 2 of Dictyostelium.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC117178; AAM44388.1; -;
DR InterPro; IPR001064; Crystallin.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
KW Hypothetical protein.
SQ SEQUENCE 229 AA; 27735 MW; FDCIE5C8B9647DD6 CRC64;

Query Match 79.2%; Score 38; DB 5; Length 229;
Best Local Similarity 66.7%; Pred. NO. 34;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLJQLKK 9
| | | | : | |
Db 119 KKWLTEIKK 127

RESULT 3

Q821K3
ID Q821K3 PRELIMINARY; PRT; 189 AA.
AC Q821K3;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Putative membrane protein.
GN STY4561.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE-21534947; PubMed-11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.F.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jaqels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL627282; CAD09337.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 189 AA; 22077 MW; C817745ABC69BE2A CRC64;

Query Match 77.1%; Score 37; DB 16; Length 189;
Best Local Similarity 66.7%; Pred. NO. 44;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLJQLKK 9
| : | | | | |
Db 101 KKWLQAKR 109

RESULT 4

Q9JYL8
ID Q9JYL8 PRELIMINARY; PRT; 275 AA.
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Phytoene synthase-related protein.
GN NMB1521.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE-20175755; PubMed-10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Winn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Citti H., Clark E.B.,
RA Cotton M.D., Otterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Pizzi M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58.";
RL Science 287:1809-1815(2000).
DR EMBL; AE002501; AAF41877.1; -;
DR TIGR; NMB1521; -;
DR InterPro; IPR002060; Squ/phyt_synthse.
DR Pfam; PF00494; SQS_PSY; 1.
KW Complete proteome.
SQ SEQUENCE 275 AA; 30613 MW; B8B2C2D77A549EA6 CRC64;

Query Match 77.1%; Score 37; DB 16; Length 275;
Best Local Similarity 77.8%; Pred. NO. 62;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKWLJQLKK 9
| | | | | | |
Db 263 KDWLMLKK 271

RESULT 5

Q9EYA7
ID Q9EYA7 PRELIMINARY; PRT; 89 AA.
AC Q9EYA7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Kil protein.
GN KIL.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7;
RX MEDLINE-20564182; PubMed-11111050;
RA Yokoyama K., Makino K., Kubota Y., Watanabe M., Kimura S.,
RA Yutsudo C.H., Kurokawa K., Ishii K., Hattori M., Abe H., Iida T.,
RA Yamamoto K., Hayashi T., Yasunaga T., Honda T., Sasakawa C.,
RA Shinagawa H.;
RT "Complete nucleotide sequence of the defective Sakai-VT1 prophage
carrying the shiga toxin 1 genes of the enterohemorrhagic Escherichia
coli O157:H7 derived from the Sakai outbreak.";
RL Gene 258:127-139(2000).
DR EMBL; AP000400; BAB19614.1; -;
SQ SEQUENCE 89 AA; 10127 MW; CD30904BF080D5FD CRC64;

Query Match 75.0%; Score 36; DB 2; Length 89;
Best Local Similarity 55.6%; Pred. NO. 33;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLIQLKK 9
| | | : | | :
Db 74 KKWILMLKR 82

RESULT 6
Q9UJ05 PRELIMINARY; PRT: 278 AA.
AC Q9UJ05;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE DJ486I3.1 (Novel protein) (Fragment).
GN DJ486I3.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL050331; CAB55880.1; -.
FT NON_TER 1
SQ SEQUENCE 278 AA; 31677 MW; 0088AF6B3BC3F6F CRC64;

Query Match 75.0%; Score 36; DB 4; Length 278;
Best Local Similarity 87.5%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLIQLK 8
| | | | | | |
Db 25 KKWLRQLK 32

RESULT 7
Q96BV3 PRELIMINARY; PRT: 284 AA.
AC Q96BV3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bladder;
RA Strausberg K.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015138; AAH15138.1; -.
KW Hypothetical protein.
SQ SEQUENCE 284 AA; 32370 MW; BCD8F0A67699530A CRC64;

Query Match 75.0%; Score 36; DB 4; Length 284;
Best Local Similarity 87.5%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKWLIQLK 8
| | | | | | |
Db 31 KKWLRQLK 38

RESULT 8
Q8H3G5 PRELIMINARY; PRT: 459 AA.
AC Q8H3G5;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE OSJNB0062D12.24 protein.
GN OSJNB0062D12.24.
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
clone:OSJNB0062D12.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP005127; BAC16708.1; -.
SQ SEQUENCE 459 AA; 51464 MW; 5D66AF12D91CF90F CRC64;

Query Match 75.0%; Score 36; DB 10; Length 459;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KWLQLKK 9
| | | : | | :
Db 322 KWLQKK 329

RESULT 9
O23488 PRELIMINARY; PRT: 578 AA.
ID O23488;
AC O23488;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein (LET1 like protein).
GN AT4G16440.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98121113; PubMed=9461215;
RA Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,
RA Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,
RA Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,
RA Wedler E., Wambutt R., Weitzenecker T., Pohl T.M., Terry N.,
RA Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
RA Auborg S., Gy I., Kreis M., Kavanagh T., Hempel S., Kottter P.,
RA Entian K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,
RA Silvey M., James R., Montfort A., Pons A., Puigdomenech P., Douka A.,
RA Voukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermaier B.,
RA Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,
RA Palme K., Benes V., Rechman S., Ansoerge W., Cooke R., Berger C.,
RA Delseny M., Voet M., Volckaert G., Mewes H.W., Klosterman S.,
RA Schueller C., Chalwatzis N.;
RT "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
Arabidopsis thaliana.";
RL Nature 391:485-488(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z97341; CAB10420.1; -.
DR EMBL: AL161544; CAB78686.1; -.
DR InterPro; IPR006459; DUF_A_thal_1569.
DR InterPro; IPR003149; Fe_hyd_SSU.
DR Pfam; PF02256; Fe_hyd_SSU; 1.
DR TIGRFAMs; TIGR01569; A_tha_TIGR01569; 1.
SQ SEQUENCE 578 AA; 64340 MW; 212385A45DC3C09A CRC64;

Query Match 75.0%; Score 36; DB 10; Length 578;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;

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Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KWLIQLKK 9
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Db 30 KWLDQLKK 37

RESULT 10
Q8I427 PRELIMINARY; PRT; 652 AA.
AC Q8I427;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cell differentiation protein rcd1, putative.
GN PFE0375W.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,
RA Hall N., Bowman S., Churcher C., Quail M., Barrell B.,
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RL
RP SEQUENCE FROM N.A.
RX MEDLINE=2225708; PubMed=12368867;
RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Howman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajadream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith K., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrell B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."
RL Nature 419:527-531(2002).
DR EMBL: AL929351; CAD51441.1; -.
SQ SEQUENCE 652 AA; 73423 MW; 90BFF62FBF7E7FFF CRC64;

Query Match 75.0%; Score 36; DB 5; Length 652;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KWLIQL 7
   ||| ||
Db 482 KWLLQL 488

RESULT 11
Q9N3E9 PRELIMINARY; PRT; 1566 AA.
AC Q9N3E9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 180.6 kDa protein.
GN Y54E10A.11.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
```

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RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Wollam A., Becker M., Graves T., Hawkins M.;
RT "The sequence of C. elegans cosmid Y54E10A.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC024810; AAF60772.2; -.
DR WormPep; Y54E10A.11; CE29120.
DR InterPro; IPR001841; Znf_ring.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50089; 2F_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 1566 AA; 180607 MW; F7D21D6EC9BA0F16 CRC64;

Query Match 75.0%; Score 36; DB 5; Length 1566;
Best Local Similarity 85.7%; Pred. No. 4.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KWLIQL 7
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Db 1477 KWLLQL 1483

RESULT 12
Q8EI76 PRELIMINARY; PRT; 136 AA.
AC Q8EI76;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN SO0971.
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MR-1;
RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Nealon K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL: AE015542; AAN54045.1; -.
DR rIGR; SO0971; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 136 AA; 15529 MW; 420710910979605C CRC64;

Query Match 72.9%; Score 35; DB 16; Length 136;
Best Local Similarity 85.7%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KWLIQLK 8
   : ||| |||
Db 69 RWLIQLK 75
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RESULT 13
O65062
ID O65062 PRELIMINARY; PRT: 198 AA.
AC O65062;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rac-like GTP binding protein.
GN SB30.
OS Picea mariana (Black spruce).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98278823; PubMed=9611216;
RA Perry D.J., Bousquet J.;
RT "Sequence-tagged-site (STS) markers of arbitrary genes. Development,
RT characterization and analysis of linkage in black spruce.";
RL Genetics 149:1089-1098(1998).
CC -1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
DR EMBL; AF051223; AAC32124.1; -.
DR HSSP; P21181; 1AM4.
DR InterPro; IPR003578; GTPase_Rho.
DR InterPro; IPR001806; Ras_trnsfrmng.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00071; ras; 1.
DR PRINTS; PR00449; RASTRNSFRMNG.
DR SMART; SM00174; RHO; 1.
DR TIGRFAMS; TIGR00231; small_GTP; 1.
KW GTP-binding; Lipoprotein; Prenylation.
SQ SEQUENCE 198 AA; 21997 MW; FA72F6EBBID15E45 CRC64;

Query Match 72.9%; Score 35; DB 10; Length 198;
Best Local Similarity 62.5%; Pred. No. 1.1e-02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKWLQLK 8
| | | | | : |
DB 98 KKWLLELR 105

RESULT 14
Q9CNC3
ID Q9CNC3 PRELIMINARY; PRT: 261 AA.
AC Q9CNC3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein PM0509.
GN PM0509.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li I.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006086; AAK02593.1; -.
DR InterPro; IPR002654; Glyco_trans_25.
DR Pfam; PF01755; Glyco_transf_25; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 261 AA; 30190 MW; 6D71C37C615EEF45 CRC64;

Query Match 72.9%; Score 35; DB 16; Length 261;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:19 ; Search time 38.625 Seconds
(without alignments)
36.985 Million cell updates/sec

Title: US-09-881-490-191
Perfect score: 51
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY:

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 51 | 100.0 | 9 | 17 | AAW04050 Antifungal peptide |
| 2 | 51 | 100.0 | 9 | 18 | AAW44590 Anti-fungal peptid |
| 3 | 51 | 100.0 | 9 | 18 | AAW44591 Anti-fungal peptid |
| 4 | 51 | 100.0 | 9 | 20 | AAW00567 Antifungal peptide |
| 5 | 51 | 100.0 | 9 | 20 | AAW00568 Antifungal peptide |
| 6 | 51 | 100.0 | 9 | 22 | AAW65491 Anti-fungal peptid |
| 7 | 51 | 100.0 | 9 | 22 | AAW65492 Anti-fungal peptid |
| 8 | 51 | 100.0 | 11 | 17 | AAW04051 Antifungal peptide |
| 9 | 51 | 100.0 | 11 | 18 | AAW44592 Anti-fungal peptid |

| | | | | | |
|----|----|-------|------|----|-----------------------------|
| 10 | 51 | 100.0 | 11 | 20 | AAW00569 Antifungal peptide |
| 11 | 51 | 100.0 | 11 | 22 | AAB65493 Anti-fungal peptid |
| 12 | 39 | 76.5 | 316 | 22 | AAG72962 Human olfactory re |
| 13 | 39 | 76.5 | 731 | 22 | AAM80128 Human protein SEQ |
| 14 | 39 | 76.5 | 731 | 22 | AAM41909 Human polypeptide |
| 15 | 39 | 76.5 | 751 | 22 | AAM40123 Human polypeptide |
| 16 | 39 | 76.5 | 875 | 22 | AAM79144 Human protein SEQ |
| 17 | 39 | 76.5 | 886 | 24 | AAE33484 Human REMAP-15 pro |
| 18 | 39 | 76.5 | 944 | 24 | ABP96125 Phoma betae aphidi |
| 19 | 39 | 76.5 | 1600 | 22 | AAE05958 Human phospholipas |
| 20 | 39 | 76.5 | 1624 | 22 | AAE05956 Human phospholipas |
| 21 | 38 | 74.5 | 313 | 22 | AAG72999 Olfactory receptor |
| 22 | 37 | 72.5 | 37 | 23 | ABG99477 Conus sp conotoxin |
| 23 | 37 | 72.5 | 37 | 23 | ABG99773 Conus sp conotoxin |
| 24 | 37 | 72.5 | 56 | 22 | AAU14900 Novel bone marrow |
| 25 | 37 | 72.5 | 79 | 23 | ABG99476 Conus sp conotoxin |
| 26 | 37 | 72.5 | 217 | 22 | AAG73054 Olfactory receptor |
| 27 | 37 | 72.5 | 217 | 22 | AAG73055 Olfactory receptor |
| 28 | 37 | 72.5 | 217 | 22 | AAG73057 Olfactory receptor |
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| 30 | 36 | 70.6 | 24 | 20 | AAW45373 Human secreted pro |
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| 32 | 36 | 70.6 | 78 | 20 | AAW13168 Human secreted pro |
| 33 | 36 | 70.6 | 117 | 23 | ABB89613 Human polypeptide |
| 34 | 36 | 70.6 | 129 | 22 | ABG07357 Novel human diagno |
| 35 | 36 | 70.6 | 133 | 22 | ABG22837 Novel human diagno |
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| 38 | 36 | 70.6 | 215 | 21 | AAB03805 Human glutathione- |
| 39 | 36 | 70.6 | 215 | 22 | AAB68866 Human glutathione- |
| 40 | 36 | 70.6 | 243 | 23 | AAE25017 Human drug metabol |
| 41 | 36 | 70.6 | 262 | 22 | AAW25798 Human protein sequ |
| 42 | 36 | 70.6 | 476 | 22 | ABB66584 Drosophila melanog |
| 43 | 36 | 70.6 | 1855 | 20 | AAW21804 Reading frame 1 pr |
| 44 | 36 | 70.6 | 1855 | 21 | AAW83272 Polypeptide encode |
| 45 | 35 | 68.6 | 61 | 22 | AAU45498 Propionibacterium |

ALIGNMENTS

RESULT :
AAW04050
ID AAW04050 standard; peptide; 9 AA.
XX
AC AAW04050;
XX
DT 04-NOV-1996 (first entry)
XX
DE Antifungal peptide XMP.360/XMP.361.
XX

Antifungal peptide; inhibitor; Domain III; polymorphonuclear leukocyte;
bactericidal/permeability-increasing protein; BPI; mammalian; PMN; fungi;
neutrophil; replication inhibitor; fungal infection; Aspergillus;
Cryptococcus; Candida; C.albicans; C.galabrat; C.krusei; C.lusitaniae;
C.parapsilosis; C.tropicalis; therapy.

| | | |
|----|-------------------|------------------------------------|
| OS | Synthetic. | |
| XX | | |
| XX | | |
| FT | Key | Location/Qualifiers |
| FT | Misc-difference 1 | /note= "D-form residue" |
| FT | Misc-difference 2 | /note= "optionally D-form residue" |
| FT | Modified-site 9 | /note= "amidated D-form residue" |
| FT | | |
| XX | | |
| PN | WO9608509-A1. | |
| XX | | |
| PD | 21-MAR-1996. | |
| XX | | |
| PF | 20-JUL-1995; | 95WO-US09262. |
| XX | | |

PR 13-JAN-1995; 95US-0372105.
PR 15-SEP-1994; 94US-0306473.
XX (XOMA) XOMA CORP.
XX Fadem MB, Lim E, Little RG;
PI WPI; 1996-179900/18.

DR Anti-fungal peptide(s) derived from Domain III of BPI protein - used
XX in vitro for killing or inhibiting replication of fungi, esp.
XX Candida species
XX Claim 13; Page 167; 199pp; English.

XX AAW04000-W04160 represent antifungal peptides. These sequences are
CC based on (or derived from) Domain III of the
CC bactericidal/permeability-increasing protein (BPI). BPI is a protein
CC that can be isolated from the granules of mammalian polymorphonuclear
CC leukocytes (PMNs or neutrophils). These antifungal peptides can be used
CC for killing, or inhibiting replication of, fungi in vitro. These
CC sequences can also be used for treatment of a fungal infection involving
CC fungi from the species Candida, Aspergillus and Cryptococcus. The
CC sequences are especially useful for treating C.albicans, C.galabrat,
CC C.krusei, C.lusitaniae, C.parapsilosis and C.tropicalis infections.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCLIQLECK 9
DB 1 KCLIQLECK 9

RESULT 2

AAW44590
ID AAW44590 standard; peptide; 9 AA.

XX AC AAW44590;

DT 27-APR-1998 (first entry)

XX Anti-fungal peptide #191 based on BPI protein (residues 142-169).

DE Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.

XX Synthetic.
OS Mammalia.

XX Key Location/Qualifiers

FH Misc-difference 1 /note= "D-form residue"

FT Misc-difference 2 /note= "D-form residue"

FT Modified-site 9 /note= "C-terminal amide, D-form residue"

XX WO9704008-A1.

XX 06-FEB-1997.

XX 21-MAR-1996; 96WO-US03845.

XX 20-JUL-1995; 95US-0504841.

XX (XOMA) XOMA CORP.

XX Fadem MB, Lim E, Little RG;

XX

DR WPI; 1997-132578/12.
XX Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides
XX Claim 1; Page 204; 230pp; English.

XX This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCLIQLECK 9
DB 1 KCLIQLECK 9

RESULT 3

AAW44591
ID AAW44591 standard; peptide; 9 AA.

XX AC AAW44591;

XX 27-APR-1998 (first entry)

XX Anti-fungal peptide #192 based on BPI protein (residues 142-169).

DE Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.

XX Synthetic.
OS Mammalia.

XX Key Location/Qualifiers

FH Misc-difference 1 /note= "D-form residue"

FT Modified-site 9 /note= "C-terminal amide, D-form residue"

XX WO9704008-A1.

XX 06-FEB-1997.

XX 21-MAR-1996; 96WO-US03845.

XX 20-JUL-1995; 95US-0504841.

XX (XOMA) XOMA CORP.

XX Fadem MB, Lim E, Little RG;

XX WPI; 1997-132578/12.

XX Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides

XX Claim 1; Page 204; 230pp; English.

XX This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or

CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.

Query Match 100.0%; Score 51; DB 18; length 9;
Best Local Similarity 100.0%; Pred. NC. 9.3e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLIQLFCK 9
| | | | | | | | | |
Db 1 KCLIQLFCK 9

RESULT 4
 AAY00567
 ID AAY00567 standard; Peptide; 9 AA.
 XX
 AC AAY00567;
 XX
 DT 07-MAY-1999 (first entry)
 XX
 DE Antifungal peptide XMP.360.
 XX
 KW Antifungal; BPI; bactericidal/permeability increasing protein;
 KW Candida infection.

```

Q      Sequence      9 AA;
Query Match      100.0%;      Score 51;      DB 20;      Length 9;
Best Local Similarity      100.0%;      Pred. No. 9.3e+05;
Matches      9;      Conservative      0;      Mismatches      0;      Indels      0;      Gaps      0;

```

```

QY      1 KCLIQLFCK 9
        |||||
Db      1 KCLIQLFCK 9

RESULT 5
AAY00568
ID      AAY00568 standard; Peptide; 9 AA.
XX
AC      AAY00568;
XX
DT      07-MAY-1999 (first entry)
XX
DE      Antifungal peptide XMP.361.

```

| | | | | |
|-----------------------|-----------------|--------------------|-----------|-----------|
| Query Match | 100.0%; | Score 51; | DB 20; | Length 9; |
| Best Local Similarity | 100.0%; | Pred. No. 9.3e+05; | | |
| Matches 9; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| QY | 1 | KCLIQLFCK | 9 | |
| | | | | |
| Db | 1 | KCLIQLFCK | 9 | |

RESULT 6
AAB65491
ID AAB65491 standard; Peptide: 9 AA.
XX
AC AAB65491;

Sequence 9 AA;

XX 27-MAR-2001 (first entry)
DT
XX
DE Anti-fungal peptide XMP.360.
XX
XX Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;
KW bactericidal/permeability-increasing protein; bactericidal;
KW fungal infection.
XX
XX Homo sapiens.
OS
XX US6156730-A.
PN
XX 05-DEC-2000.
PD
XX 08-JAN-1999; 99US-0227659.
PF
XX 21-MAR-1996; 96US-0621259.
PR 12-MAR-1993; 93US-0030644.
PR 15-JUL-1993; 93US-0093202.
PR 14-JAN-1994; 94US-0183222.
PR 11-MAR-1994; 94US-0209762.
PR 11-JUL-1994; 94US-0273540.
PR 15-SEP-1994; 94US-0306473.
PR 13-JAN-1995; 95US-0372105.
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Lim E, Fadem MB, Little RG;
XX
DR WPI; 2001-090160/10.
XX
PT Novel anti-fungal peptides derived from domain III of
PT bactericidal/permeability-increasing protein useful for killing or
PT inhibiting replication of fungi and for treating fungal infections -
XX
PS Example 2; Columns 191-192; 134pp; English.
XX
CC The present invention relates to antifungal peptides (see
CC AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C.albicans, C.glabrata, C.krusei,
CC C.lusitanae, C.parapsilosis and C.tropicalis.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 51; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KCLIQLFCK 9
Db 1 KCLIQLFCK 9
RESULT 7
AAB65492
ID AAB65492 standard; Peptide: 9 AA.
XX
AC AAB65492;
XX
DT 27-MAR-2001 (first entry)
XX
DE Anti-fungal peptide XMP.361.
XX
KW Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;

KW bactericidal/permeability-increasing protein; bactericidal;
KW fungal infection.
XX
OS Homo sapiens.
XX
PN US6156730-A.
XX
PD 05-DEC-2000.
XX
PF 08-JAN-1999; 99US-0227659.
XX
PR 21-MAR-1996; 96US-0621259.
PR 12-MAR-1993; 93US-0030644.
PR 15-JUL-1993; 93US-0093202.
PR 14-JAN-1994; 94US-0183222.
PR 11-MAR-1994; 94US-0209762.
PR 11-JUL-1994; 94US-0273540.
PR 15-SEP-1994; 94US-0306473.
PR 13-JAN-1995; 95US-0372105.
PR 20-JUL-1995; 95US-0504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Lim E, Fadem MB, Little RG;
XX
DR WPI; 2001-090160/10.
XX
PT Novel anti-fungal peptides derived from domain III of
PT bactericidal/permeability-increasing protein useful for killing or
PT inhibiting replication of fungi and for treating fungal infections -
XX
PS Example 2; Columns 193-194; 134pp; English.
XX
CC The present invention relates to antifungal peptides (see
CC AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C.albicans, C.glabrata, C.krusei,
CC C.lusitanae, C.parapsilosis and C.tropicalis.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 51; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Caps 0;
QY 1 KCLIQLFCK 9
Db 1 KCLIQLFCK 9
RESULT 8
AAW04051
ID AAW04051 standard; peptide; 11 AA.
XX
AC AAW04051;
XX
DT 04-NOV-1996 (first entry)
XX
DE Antifungal peptide XMP.362.
XX
KW Antifungal peptide; inhibitor; Domain III; polymorphonuclear leukocyte;
KW bactericidal/permeability-increasing protein; BPI; mammalian; PMN; fungi;
KW neutrophil; replication inhibitor; fungal infection; Aspergillus;
KW Cryptococcus; Candida; C.albicans; C.glabrat; C.krusei; C.lusitanae;
KW C.parapsilosis; C.tropicalis; therapy.
XX
OS Synthetic.

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XX FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT FT Modified-site 11
FT FT /note= "amidated D-form residue"
XX XX WO9608509-A1.
XX XX 21-MAR-1996.
PD XX
XX XX 20-JUL-1995; 95WO-US09262.
XX XX
PR 13-JAN-1995; 95US-0372105.
PR 15-SEP-1994; 94US-0306473.
XX XX
PA (XOMA ) XOMA CORP.
XX XX
PI Fadem MB, Lim E, Little RG;
XX XX
DR WPI; 1996-179900/18.
XX XX
PT Antifungal peptide(s) derived from Domain III of BPI protein - used
PT in vitro for killing or inhibiting replication of fungi, esp.
PT Candida species
XX XX
PS Claim 13; Page 168; 199pp; English.
XX XX
CC AAW04000-W04160 represent antifungal peptides. These sequences are
CC based on (or derived from) Domain III of the
CC bactericidal/permeability-increasing protein (BPI). BPI is a protein
CC that can be isolated from the granules of mammalian polymorphonuclear
CC leukocytes (PMNs or neutrophils). These antifungal peptides can be used
CC for killing, or inhibiting replication of, fungi in vitro. These
CC sequences can also be used for treatment of a fungal infection involving
CC fungi from the species Candida, Aspergillus and Cryptococcus. The
CC sequences are especially useful for treating C.albicans, C.galabrat,
CC C.krusei, C.lusitanlae, C.parapsilosis and C.tropicalis infections.
XX XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 51; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KCLIQLFCK 9
Db 2 KCLIQLFCK 10
RESULT 9
AAW44592
ID AAW44592 standard; peptide; 11 AA.
XX XX
AC AAW44592;
XX XX
DT 27-APR-1998 (first entry)
XX XX
DE Anti-fungal peptide #193 based on Bpi protein (residues 142-169).
XX XX
KW Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.
XX XX
OS Synthetic.
OS Mammalia.
XX XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT FT Modified-site 11 /note= "C-terminal amide, D-form residue"
FT FT
XX XX WO9704008-A1.

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XX PD 06-FEB-1997.
XX XX
PF 21-MAR-1996; 96WO-US03845.
XX XX
PR 20-JUL-1995; 95US-0504841.
XX XX
PA (XOMA ) XOMA CORP.
XX XX
PI Fadem MB, Lim E, Little RG;
XX XX
DR WPI; 1997-132578/12.
XX XX
PT Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or
PT in vivo as a fungicides
XX XX
PS Claim 1; Page 205; 230pp; English.
XX XX
CC This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices.
XX XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 51; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KCLIQLFCK 9
Db 2 KCLIQLFCK 10
RESULT 10
AAY00569
ID AAY00569 standard; Peptide; 11 AA.
XX XX
AC AAY00569;
XX XX
DT 07-MAY-1999 (first entry)
XX XX
DE Antifungal peptide XMP.362.
XX KW
KW Antifungal; BPI; bactericidal/permeability increasing protein;
KW Candida infection.
XX XX
OS Synthetic.
XX XX
PN US5858974-A.
XX XX
PD 12-JAN-1999.
XX XX
PF 21-MAR-1996; 96US-0621259.
XX XX
PR 21-MAR-1996; 96US-0621259.
PR 20-JUL-1995; 95US-0504841.
XX XX
PA (XOMA ) XOMA CORP.
XX XX
PI Fadem MB, Lim E, Little RG;
XX XX
DR WPI; 1999-119956/10.
XX XX
PT Antifungal peptides - comprising part of bactericidal or
PT permeability-increasing protein sequence or related sequence
XX XX
PS Disclosure; Columns 187-188; 132pp; English.
XX XX

```

CC New peptides are provided which are based on Domain III (amino acids
CC 142-169) of human bactericidal/permeability-increasing protein (BPI).
CC The peptides all have a C-terminal amide. More particularly, the Claims
CC relate to: (1) a peptide that has an amino acid sequence of human BPI
CC from position 148 to position 161 (KSKVGMWQLFHKK) and variants of the
CC sequence having antifungal activity; and (2) an antifungal peptide
CC having 6-14 amino acids comprising (a) a core sequence selected from
CC LIQL, IQLF, WLQL, LIQLF and WLQLF and (b) one or more cationic amino
CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric
CC acid) at the N and/or C terminus of the core sequence. The new peptides
CC are used for killing or inhibiting replication of fungi in vitro; and
CC for treating fungal infections in vivo, in particular infections of
CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.
CC krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide
CC can be administered topically, intravenously, orally or as an aerosol,
CC optionally together with a non-peptide antifungal agent.

XX SQ Sequence 11 AA;
SQ Query Match 100.0%; Score 51; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 9
Db 2 KCLIQLFCK 10

RESULT 11
AAB65493
ID AAB65493 standard; Peptide; 11 AA.

XX AC AAB65493;
XX 27-MAR-2001 (first entry)
XX Anti-fungal peptide XMP.362.
DE Human; BPI; antifungal; polymorphonuclear leukocyte; neutrophil;
XX bactericidal/permeability-increasing protein; bactericidal;
KW fungal infection.
KW Homo sapiens.
XX US6156730-A.
XX 05-DEC-2000.
XX 08-JAN-1999; 99US-0227659.
XX 21-MAR-1996; 96US-0621259.
PR 12-MAR-1993; 93US-0030644.
PR 15-JUL-1993; 93US-0093202.
PR 14-JAN-1994; 94US-0183222.
PR 11-MAR-1994; 94US-0209762.
PR 11-JUL-1994; 94US-0273540.
PR 15-SEP-1994; 94US-0306473.
PR 13-JAN-1995; 95US-0372105.
PR 20-JUL-1995; 95US-0504841.

XX (XOMA) XOMA CORP.
XX Llm E, Fadem MB, Little RG;
XX WPI; 2001-090160/10.
XX Novel anti-fungal peptides derived from domain III of
PT bactericidal/permeability-increasing protein useful for killing or
PT inhibiting replication of fungi and for treating fungal infections -
XX Example 2; Columns 193-194; 134pp; English.
PS The present invention relates to antifungal peptides (see

CC AAB65301-B65550) derived from Domain III (amino acids 142-169) of
CC bactericidal/permeability-increasing protein (BPI). The present sequence
CC is one such antifungal peptide. BPI is a protein isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or
CC neutrophils). BPI has potent bactericidal activity against a broad range
CC of gram-negative bacteria. The peptides of the present invention are
CC useful for killing or inhibiting replication of fungi, and treating
CC infections caused by fungus belonging to Candida, Aspergillus,
CC Cryptococcus species such as C. albicans, C. glabrata, C. krusei,
CC C. lusitanae, C. parapsilosis and C. tropicalis.

XX SQ Sequence 11 AA;
SQ Query Match 100.0%; Score 51; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 9
Db 2 KCLIQLFCK 10

RESULT 12
AAG72962
ID AAG72962 standard; Protein; 316 AA.

XX AC AAG72962;
XX 30-JUL-2001 (first entry)
XX Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2644.
KW Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation;
KW human olfactory receptor data exploratorium; HORDE.

XX Homo sapiens.

XX WO200127158-A2.

XX 19-APR-2001.

XX 06-OCT-2000; 2000WO-US27582.

XX 08-OCT-1999; 99US-0158615.

XX 24-FEB-2000; 2000US-0184809.

XX (DIGI-) DIGISCENTS.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Rellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

XX WPI; 2001-290713/30.

XX New polynucleotides which encode polypeptides involved in olfactory
XX sensation for identifying olfactory agonists and antagonists -
XX Example 6; Page 1787-1788; 1857pp; English.

XX The present sequence is a polypeptide from the human olfactory receptor
XX data exploratorium (HORDE). It was used as a query sequence in a database
XX search of olfactory receptor (OR)-like sequences. The invention relates
XX to isolated polynucleotides encoding polypeptides involved in olfactory
XX sensation. The polynucleotides can be used in screening for olfactory
XX agonists and antagonists. The methods allow for the determination of
XX primary scents and the identification of the odour receptors used to
XX detect these primary scents. The methods also enable determination of
XX secondary scents and the identification of combinations of odour
XX receptors that are involved in detecting such secondary scents. This
XX enables the construction of a scent representation (also called a scent
XX fingerprint or scent profile), which may be used to re-create and edit
XX scents. Libraries of olfactory receptors are useful for determining the

CC interaction pattern of a composition with the receptors, and can be
CC used for determining differences in the olfactory faculties of different
CC individuals.
XX
SQ Sequence 316 AA;

Query Match 76.5%; Score 39; DB 22; Length 316;
Best Local Similarity 85.7%; Pred. NO. 70;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 CLIQLFC 8
Db 99 CLIQMFC 105

RESULT 13
AAM80128
ID AAM80128 standard; Protein; 731 AA.
XX
AC AAM80128;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 3774.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cac Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK53261.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 432-433; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666

CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 731 AA;

Query Match 76.5%; Score 39; DB 22; Length 731;
Best Local Similarity 75.0%; Pred. NO. 1.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 CLIQLFCK 9
Db 466 CLIQLYCE 473

RESULT 14
AAM41909
ID AAM41909 standard; Protein; 731 AA.
XX
AC AAM41909;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 6840.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI61065.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Example 2; SEQ ID NO 6840; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 731 AA;

Query Match 76.5%; Score 39; DB 22; Length 731;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 CLIQLFCK 9
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Db 466 CLIQLYCE 473

RESULT 15
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ID AAM40123 standard; Protein; 751 AA.
XX
AC AAM40123;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 3268.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI59279.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Example 5; SEQ ID NO 3268; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 751 AA;

Query Match 76.5%; Score 39; DB 22; Length 751;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 CLIQLFCK 9
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Db 486 CLIQLYCE 493

Search completed: October 14, 2003, 14:41:34
Job time : 40.7917 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:23 ; Search time 12.75 Seconds
(without alignments)
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Title: US-09-881-490-191
Perfect score: 51
Sequence: 1 KCLIQ.FCK 9

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Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
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| 1 | 51 | 100.0 | 9 | 2 US-08-621-259A-191 | Sequence 191, App |
| 2 | 51 | 100.0 | 9 | 2 US-08-621-259A-192 | Sequence 192, App |
| 3 | 51 | 100.0 | 9 | 5 PCT-US95-09262-191 | Sequence 191, App |
| 4 | 51 | 100.0 | 9 | 5 PCT-US95-09262-192 | Sequence 192, App |
| 5 | 51 | 100.0 | 11 | 2 US-08-621-259A-193 | Sequence 193, App |
| 6 | 51 | 100.0 | 11 | 5 PCT-US95-09262-193 | Sequence 193, App |
| 7 | 36 | 70.6 | 78 | 3 US-08-905-223-452 | Sequence 452, App |
| 8 | 36 | 70.6 | 215 | 2 US-08-941-263-1 | Sequence 1, Appli |
| 9 | 36 | 70.6 | 215 | 3 US-09-227-178-1 | Sequence 1, Appli |
| 10 | 36 | 70.6 | 215 | 3 US-09-470-449-1 | Sequence 1, Appli |
| 11 | 36 | 70.6 | 215 | 4 US-09-726-775-1 | Sequence 1, Appli |
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| 25 | 32 | 62.7 | 29 | 3 US-08-871-355A-304 | Sequence 304, App |
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| 38 | 32 | 62.7 | 815 | 4 US-09-914-259-18 | Sequence 18, Appli |
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| 41 | 31 | 60.8 | 479 | 4 US-09-442-100-13 | Sequence 13, Appli |
| 42 | 31 | 60.8 | 479 | 4 US-08-939-106-13 | Sequence 13, Appli |
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| 44 | 31 | 60.8 | 605 | 2 US-08-889-402-2 | Sequence 2, Appli |
| 45 | 31 | 60.8 | 795 | 3 US-09-031-563-23 | Sequence 23, Appli |

ALIGNMENTS

RESULT 1
US-08-621-259A-191
; Sequence 191, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.360"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1 & 9
; OTHER INFORMATION: /label= D-Lys
; OTHER INFORMATION: /note= "Positions 1 & 9 are D-lysine."

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; NAME/KEY: Modified-site
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; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-191

Query Match 100.0%; Score 51; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 9
Db 1 KCLIQLFCK 9

RESULT 2
US-08-621-259A-192
; Sequence 192, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 192:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.361"
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; NAME/KEY: Modified-site
; LOCATION: 1 & 9
; OTHER INFORMATION: /label= D-Lys
; OTHER INFORMATION: /note= "Positions 1 & 9 are D-lysine."
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; NAME/KEY: Modified-site
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; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-192

Query Match 100.0%; Score 51; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 9
Db 1 KCLIQLFCK 9

RESULT 3
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; Sequence 191, Application PC/TUS9509262
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09262
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/10040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
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OTHER INFORMATION: "XMP.360"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1 & 9
OTHER INFORMATION: /label- D-Lys
OTHER INFORMATION: /note= "Positions 1 & 9 are D-lysine."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /label- D-Cys
OTHER INFORMATION: /note= "Position 2 is D-cysteine."
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label- Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-191

Query Match 100.0%; Score 51; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLIQLFCK 9
Db 1 KCLIQLFCK 9

RESULT 4
PCT-US95-09262-192
Sequence 192, Application PC/TUS9509262
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Anti-Fungal Peptides
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09262
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/372,105
FILING DATE: 13-JAN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/306,473
FILING DATE: 15-SEP-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/093,202
FILING DATE: 15-JUL-93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030,644
FILING DATE: 12-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27129/10040
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 192:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: "XMP.361"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1 & 9
OTHER INFORMATION: /label- D-Lys
OTHER INFORMATION: /note= "Positions 1 & 9 are D-lysine."
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label- Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-192

Query Match 100.0%; Score 51; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLIQLFCK 9
Db 1 KCLIQLFCK 9

RESULT 5
US-08-621-259A-193
Sequence 193, Application US/08621259A
Patent No. 5858974
GENERAL INFORMATION:
APPLICANT: Little II, Roger G
APPLICANT: Lim, Edward
APPLICANT: Fadem, Mitchell B.
TITLE OF INVENTION: Anti-Fungal Peptides
NUMBER OF SEQUENCES: 252
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,259A
FILING DATE: 21-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/504,841
FILING DATE: 20-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11021US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX:
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.362"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-193

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Best Local Similarity 100.0%; Pred. No. 0.0092;
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QY 1 KCLIQLFCK 9
Db 2 KCLIQLFCK 10

RESULT 6
PCT-US95-09262-193
Sequence 193, Application PC/TUS9509262
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Anti-Fungal Peptides
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09262
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/372,105
FILING DATE: 13-JAN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/306,473
FILING DATE: 15-SEP-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/093,202
FILING DATE: 15-JUL-93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030,644
FILING DATE: 12-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.

REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/10040
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.362"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-193

Query Match 100.0%; Score 51; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 9
Db 2 KCLIQLFCK 10

RESULT 7
US-08-905-223-452
Sequence 452, Application US/08905223
Patent No. 6222029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duclert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 452:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: AMINO ACID

TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
TISSUE TYPE: Brain
FEATURE:
NAME/KEY: sig_peptide
LOCATION: -69...
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 5.7
OTHER INFORMATION: seq LCRLCLVRLFC/SS
US-08-905-223-452

Query Match 70.6%; Score 36; DB 3; Length 78;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 CLLIQLPC 8

Db 62 CLVRLFC 68

RESULT 8

US-08-941-263-1
; Sequence 1, Application US/08941263
; Patent No. 5962231
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN GLUTATHIONE-S-TRANSFERASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,263
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0398 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRSTNOT16
CLONE: 3037341

Query Match 70.6%; Score 36; DB 2; Length 215;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 9

Db 86 KMLLELFCK 94

RESULT 9

US-09-227-178-1
; Sequence 1, Application US/09227178
; Patent No. 6071513
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN GLUTATHIONE-S-TRANSFERASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,178
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/941,263
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0398 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRSTNOT16
CLONE: 3037341

Query Match 70.6%; Score 36; DB 3; Length 215;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 9

Db 86 KMLLELFCK 94

RESULT 10

US-09-470-449-1
; Sequence 1, Application US/09470449
; Patent No. 6177546
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN GLUTATHIONE-S-TRANSFERASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto

```
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/470,449
; FILING DATE: Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/227,178
; FILING DATE: January 8, 1999
; APPLICATION NUMBER: 08/941,263
; FILING DATE: September 30, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Diana Hamlet-Cox
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: PF-0398-2 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-849-8886
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT16
; CLONE: 3037341
; US-09-470-449-1

Query Match 70.6%; Score 36; DB 3; Length 215;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 9
| | : | | |
Db 86 KMLELFLCK 94

RESULT 11
US-09-726-775-1
; Sequence 1, Application US/09726775
; Patent No. 6506571
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; Corley, Neil C.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN GLUTATHIONE-S-TRANSFERASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,775
; FILING DATE: 29-Nov-6506571-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/470,449
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/941,263
; FILING DATE: September 30, 1997
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; ATTORNEY/AGENT INFORMATION:
; NAME: Diana Hamlet-Cox
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: PF-0398-2 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-849-8886
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT16
; CLONE: 3037341
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-726-775-1

Query Match 70.6%; Score 36; DB 4; Length 215;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 9
| | : | | |
Db 86 KMLELFLCK 94

RESULT 12
US-08-766-551-9
; Sequence 9, Application US/08766551
; Patent No. 5840569
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN GTP-BINDING PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,551
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0168 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
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LIBRARY: GenBank
CLONE: 240986
US-08-766-551-9

Query Match 68.6%; Score 35; DB 2; Length 208;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CLIQLFCK 9
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Db 16 CLINRFCK 23

RESULT 13

US-09-075-454-1
; Sequence 1, Application US/09075454
; Patent No. 6391580
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Tang, Y. Tom
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Patterson, Chandra
; APPLICANT: Batra, Sajeev
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: RAS PROTEINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,454
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/766,551
; FILING DATE: DECEMBER 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0168-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNNOT05
CLONE: 627565

US-09-075-454-1

Query Match 68.6%; Score 35; DB 4; Length 259;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CLIQLFCK 9
||| |||
Db 67 CLINRFCK 74

RESULT 14

US-09-075-454-4
; Sequence 4, Application US/09075454
; Patent No. 6391580
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Tang, Y. Tom
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Patterson, Chandra
; APPLICANT: Batra, Sajeev
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: RAS PROTEINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,454
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/766,551
; FILING DATE: DECEMBER 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0168-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 260 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSTUT08
CLONE: 1651593

US-09-075-454-4

Query Match 68.6%; Score 35; DB 4; Length 260;
Best Local Similarity 75.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CLIQLFCK 9
||| |||
Db 68 CLINRFCK 75

RESULT 15

US-08-820-970-2
; Sequence 2, Application US/08820970
; Patent No. 6008022
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: SU, KUI
; APPLICANT: LI, HAODONG
; TITLE OF INVENTION: HUMAN CYTOKINE POLYPEPTIDE

```

; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,970
; FILING DATE: 20-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, Anders, A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF270
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-820-970-2

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Query Match 66.7% Score 34; DB 3; Length 223;
Best Local Similarity 66.7%; Pred. No. ic+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Oy 1 KCLIQLECK 9
Db 37 KCLIQELCQ 45

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Search completed: October 14, 2003, 14:42:47
Job time : 13.75 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2003, 14:34:14 ; Search time 21.9375 Seconds
(without alignments)
66.104 Million cell updates/sec

Title: US-09-881-490-191
Perfect score: 51
Sequence: i KCLIQLFCK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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| 2: | /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:* |
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| 9: | /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:* |
| 10: | /cgn2_6/ptodata/2/pubpaa/US09H_PUBCOMB.pep:* |
| 11: | /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:* |
| 12: | /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:* |
| 13: | /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:* |
| 14: | /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:* |
| 15: | /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:* |
| 16: | /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:* |
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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|--------------------------------------|
| 1 | 51 | 100.0 | 9 | 9 | US-09-881-490-191 Sequence 191, App |
| 2 | 51 | 100.0 | 9 | 9 | US-09-881-490-192 Sequence 192, App |
| 3 | 51 | 100.0 | 11 | 9 | US-09-881-490-193 Sequence 193, App |
| 4 | 39 | 76.5 | 291 | 11 | US-09-832-522-52 Sequence 52, Appl |
| 5 | 39 | 76.5 | 297 | 11 | US-09-832-522-34 Sequence 34, Appl |
| 6 | 39 | 76.5 | 297 | 11 | US-09-832-522-49 Sequence 49, Appl |
| 7 | 39 | 76.5 | 298 | 11 | US-09-832-522-44 Sequence 44, Appl |
| 8 | 39 | 76.5 | 319 | 11 | US-09-966-459A-11 Sequence 11, Appl |
| 9 | 37 | 72.5 | 37 | 15 | US-10-072-602B-172 Sequence 172, App |
| 10 | 37 | 72.5 | 37 | 15 | US-10-072-602B-558 Sequence 558, App |
| 11 | 37 | 72.5 | 79 | 15 | US-10-072-602B-171 Sequence 171, App |
| 12 | 36 | 70.6 | 24 | 11 | US-09-798-889-168 Sequence 168, App |
| 13 | 36 | 70.6 | 195 | 11 | US-09-798-889-164 Sequence 164, App |
| 14 | 35 | 68.6 | 197 | 10 | US-09-764-868-1119 Sequence 1119, Ap |
| 15 | 35 | 68.6 | 228 | 10 | US-09-764-868-1107 Sequence 1107, Ap |

| | | | | | | |
|----|------|------|------|----|--------------------|-------------------|
| 16 | 35 | 68.6 | 230 | 10 | US-09-764-868-685 | Sequence 685, App |
| 17 | 35 | 68.6 | 259 | 14 | US-10-051-986-1 | Sequence 1, Appli |
| 18 | 35 | 68.6 | 259 | 15 | US-10-153-668-3 | Sequence 3, Appli |
| 19 | 35 | 68.6 | 260 | 14 | US-10-051-986-4 | Sequence 4, Appli |
| 20 | 35 | 68.6 | 287 | 10 | US-09-764-868-700 | Sequence 700, App |
| 21 | 35 | 68.6 | 734 | 15 | US-10-170-528-2 | Sequence 2, Appli |
| 22 | 34 | 66.7 | 160 | 12 | US-10-017-161-1380 | Sequence 1380, Ap |
| 23 | 34 | 66.7 | 222 | 9 | US-09-897-772-2 | Sequence 2, Appli |
| 24 | 34 | 66.7 | 222 | 14 | US-10-092-925-2 | Sequence 2, Appli |
| 25 | 34 | 66.7 | 223 | 10 | US-09-811-088-8 | Sequence 8, Appli |
| 26 | 34 | 66.7 | 223 | 15 | US-10-314-410-8 | Sequence 8, Appli |
| 27 | 34 | 66.7 | 318 | 10 | US-09-886-055-101 | Sequence 101, App |
| 28 | 34 | 66.7 | 318 | 11 | US-09-804-291-101 | Sequence 101, App |
| 29 | 34 | 66.7 | 318 | 15 | US-10-081-775-5 | Sequence 5, Appli |
| 30 | 34 | 66.7 | 665 | 11 | US-09-533-029-76 | Sequence 76, Appl |
| 31 | 34 | 66.7 | 665 | 16 | US-10-278-536-100 | Sequence 100, App |
| 32 | 33.5 | 65.7 | 971 | 14 | US-10-116-048-2 | Sequence 2, Appli |
| 33 | 33.5 | 65.7 | 2471 | 14 | US-10-116-048-4 | Sequence 4, Appli |
| 34 | 33 | 64.7 | 43 | 11 | US-09-764-891-3189 | Sequence 3189, Ap |
| 35 | 33 | 64.7 | 43 | 15 | US-10-205-428-360 | Sequence 360, App |
| 36 | 33 | 64.7 | 57 | 11 | US-09-983-802-275 | Sequence 275, App |
| 37 | 33 | 64.7 | 78 | 11 | US-09-798-889-46 | Sequence 46, Appl |
| 38 | 33 | 64.7 | 87 | 9 | US-09-945-301-7 | Sequence 7, Appli |
| 39 | 33 | 64.7 | 162 | 9 | US-09-925-302-593 | Sequence 593, App |
| 40 | 33 | 64.7 | 163 | 11 | US-09-898-659-2 | Sequence 2, Appli |
| 41 | 33 | 64.7 | 163 | 11 | US-09-898-659-4 | Sequence 4, Appli |
| 42 | 33 | 64.7 | 240 | 10 | US-09-925-300-1658 | Sequence 1658, Ap |
| 43 | 33 | 64.7 | 326 | 10 | US-09-886-055-267 | Sequence 267, App |
| 44 | 33 | 64.7 | 326 | 11 | US-09-804-291-267 | Sequence 267, App |
| 45 | 33 | 64.7 | 381 | 10 | US-09-919-497-96 | Sequence 96, Appl |

ALIGNMENTS

RESULT 1
US-09-881-490-191
; Sequence 191, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94

APPLICATION NUMBER: 08/093,202
FILING DATE: 15-JUL-93
APPLICATION NUMBER: 08/030,644
FILING DATE: 12-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 100-238/11021US01
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.360"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1 & 9
OTHER INFORMATION: /label= D-Lys
/note= "Positions 1 & 9 are D-lysine."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /label= D-Cys
/note= "Position 2 is D-cysteine."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /label= D-Cys
/note= "Position 2 is D-cysteine."
SEQUENCE DESCRIPTION: SEQ ID NO: 191:
US-09-881-490-191

Query Match 100.0%; Score 51; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLIQLFCK 9
Db 1 KCLIQLFCK 9

RESULT 2
US-09-881-490-192
Sequence 192, Application US/09881490
Patent No. US20020077298A1
GENERAL INFORMATION:
APPLICANT: Little II, Roger G.
Lim, Edward
Fadem, Mitchell B.
TITLE OF INVENTION: Anti-Fungal Peptides
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th FloorDrive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/881,490
FILING DATE: 14-Jun-2001

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/119,858
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/372,105
FILING DATE: 13-JAN-95
APPLICATION NUMBER: 08/306,473
FILING DATE: 15-SEP-94
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-94
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-94
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-94
APPLICATION NUMBER: 08/093,202
FILING DATE: 15-JUL-93
APPLICATION NUMBER: 08/030,644
FILING DATE: 12-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 100-238/11021US01
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 192:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.361"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1 & 9
OTHER INFORMATION: /label= D-Lys
/note= "Positions 1 & 9 are D-lysine."
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
/note= "The C-Terminus is Amidated"
SEQUENCE DESCRIPTION: SEQ ID NO: 192:
US-09-881-490-192

Query Match 100.0%; Score 51; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLIQLFCK 9
Db 1 KCLIQLFCK 9

RESULT 3
US-09-881-490-193
Sequence 193, Application US/09881490
Patent No. US20020077298A1
GENERAL INFORMATION:
APPLICANT: Little II, Roger G.
Lim, Edward
Fadem, Mitchell B.
TITLE OF INVENTION: Anti-Fungal Peptides
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th FloorDrive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60661

```
;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.362"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1 & 11
; OTHER INFORMATION: /label= D-Lys
; /note= "Positions 1 & 11 are D-lysine."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-09-881-490-193

Query Match 100.0%; Score 51; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLIQLFCK 9
Db 2 KCLIQLFCK 10

RESULT 4
US-09-832-522-52
; Sequence 52, Application US/09832522
; Publication No. US20030091563A1
; GENERAL INFORMATION:
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Gangolli, Esha A
; APPLICANT: Rastelli, Luca
; APPLICANT: Smithson, Glennda
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Vernet, Corine
; APPLICANT: Wolenc, Adam R
; APPLICANT: Casman, Stacie J
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Szekeres, Edward S
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John P
; APPLICANT: Burgess, Catherine E
; TITLE OF INVENTION: NO. US20030091563A1el GPCR-Proteins and Nucleic Acids Encodi
```

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; APPLICANT: Padigar, Muralidhara
; APPLICANT: Vernet, Corine
; APPLICANT: Wolenc, Adam R
; APPLICANT: Casman, Stacie J
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Szekeres, Edward S
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John P
; APPLICANT: Burgess, Catherine E
; TITLE OF INVENTION: NO. US20030091563A1el GPCR-Proteins and Nucleic Acids Encodi
; FILE REFERENCE: 15966-767
; CURRENT APPLICATION NUMBER: US/09/832,522
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/195,994
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/196,538
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/220,644
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/264,851
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/199,964
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/268,567
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/199,955
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/259,641
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/200,176
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199,948
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199,956
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/218,995
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 52
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-832-522-52

Query Match 76.5%; Score 39; DB 11; Length 291;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CLIQLFCK 8
Db 79 CLIQMFC 85

RESULT 5
US-09-832-522-34
; Sequence 34, Application US/09832522
; Publication No. US20030091563A1
; GENERAL INFORMATION:
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Gangolli, Esha A
; APPLICANT: Rastelli, Luca
; APPLICANT: Smithson, Glennda
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Vernet, Corine
; APPLICANT: Wolenc, Adam R
; APPLICANT: Casman, Stacie J
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Szekeres, Edward S
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John P
; APPLICANT: Burgess, Catherine E
; TITLE OF INVENTION: NO. US20030091563A1el GPCR-Proteins and Nucleic Acids Encodi
```

```
; FILE REFERENCE: 15966-767
; CURRENT APPLICATION NUMBER: US/09/832,522
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/195,994
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/196,538
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/220,644
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/264,851
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/199,964
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/268,567
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/199,955
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/259,641
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/200,176
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199,948
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199,956
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/218,995
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-832-522-34
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Query Match 76.5%; Score 39; DB 11; Length 297;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 2 CLIQLFC 8
Db 86 CLIQMFC 92
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```
RESULT 6
US-09-832-522-49
; Sequence 49, Application US/09832522
; Publication No. US20030091563A1
; GENERAL INFORMATION:
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Gangolli, Esha A
; APPLICANT: Rastelli, Luca
; APPLICANT: Smithson, Glennda
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Vernet, Corine
; APPLICANT: Wolenc, Adam R
; APPLICANT: Casman, Stacie J
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Szekeres, Edward S
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John P
; APPLICANT: Burgess, Catherine E
; TITLE OF INVENTION: No. US20030091563A1el GPCR-Proteins and Nucleic Acids Encoding Sa
; FILE REFERENCE: 15966-767
; CURRENT APPLICATION NUMBER: US/09/832,522
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/195,994
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/196,538
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/220,644
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/264,851
```

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; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/199,964
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/268,567
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/199,955
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/259,641
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/200,176
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199,948
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199,956
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/218,995
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-832-522-49
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Query Match 76.5%; Score 39; DB 11; Length 297;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 2 CLIQLFC 8
Db 86 CLIQMFC 92
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RESULT 7

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US-09-832-522-44
; Sequence 44, Application US/09832522
; Publication No. US20030091563A1
; GENERAL INFORMATION:
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Gangolli, Esha A
; APPLICANT: Rastelli, Luca
; APPLICANT: Smithson, Glennda
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Vernet, Corine
; APPLICANT: Wolenc, Adam R
; APPLICANT: Casman, Stacie J
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Szekeres, Edward S
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John P
; APPLICANT: Burgess, Catherine E
; TITLE OF INVENTION: No. US20030091563A1el GPCR-Proteins and Nucleic Acids Encodin
; FILE REFERENCE: 15966-767
; CURRENT APPLICATION NUMBER: US/09/832,522
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/195,994
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/196,538
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/220,644
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/264,851
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/199,964
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/268,567
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/199,955
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/259,641
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/200,176
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; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199,948
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199,956
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/216,995
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-832-522-44

Query Match 76.5%; Score 39; DB 11; Length 298;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 CLIQMFC 8
 ||||:||
Db 86 CLIQMFC 92

RESULT 8

US-09-966-459A-11
; Sequence 11, Application US/09966459A
; Publication No. US2003022237A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J.N.
; APPLICANT: MINTIER, G.
; APPLICANT: RAMANATHAN, C.S.
; APPLICANT: HAWKEN, D.R.
; APPLICANT: CACACE, A.
; APPLICANT: BARBER, L.
; APPLICANT: KORNACKER, M.G.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBM4,
; FILE REFERENCE: D0039NP
; CURRENT APPLICATION NUMBER: US/09/966,459A
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,833
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,776
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/305,351
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/313,202
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 319
; TYPE: PRT
; ORGANISM: CHICKEN
US-09-966-459A-11

Query Match 76.5%; Score 39; DB 11; Length 319;
Best Local Similarity 85.7%; Pred. No. 55;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 CLIQMFC 8
 ||||:||
Db 97 CLIQMFC 103

RESULT 9

US-10-072-602B-172
; Sequence 172, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.

; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 172
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(37)
; OTHER INFORMATION: Xaa at residues 4, 7, 8, 11, 13 and 14 is Glu or gamma-carb
; OTHER INFORMATION: Glu; Xaa at residues 3 and 25 is Pro or hydroxy-Pro
US-10-072-602B-172

Query Match 72.5%; Score 37; DB 15; Length 37;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCLIQMFC 8
 ||||:||
Db 30 KCLLSIFC 37

RESULT 10

US-10-072-602B-558
; Sequence 558, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 558
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-10-072-602B-558

Query Match 72.5%; Score 37; DB 15; Length 37;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 8
| | | : | |
Db 30 KCLLSIFCK 37

RESULT 11
US-10-072-602B-171
; Sequence 171, Application US/10072602B
; Publication No. US20030109676A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 171
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-10-072-602B-171

Query Match 72.5%; Score 37; DR 15; Length 79;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 8
| | | : | |
Db 72 KCLLSIFCK 79

RESULT 12
US-09-798-889-168
; Sequence 168, Application US/09798889
; Publication No. US20030004324A:
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 31 Human secreted proteins
; FILE REFERENCE: PZ026P1
; CURRENT APPLICATION NUMBER: US/09/798,889
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/393,022
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,714
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,686
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,696
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 168
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-798-889-168

Query Match 70.6%; Score 36; DR 11; Length 24;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 9
| | | : | | | |
Db 14 KMLLELFCK 22

RESULT 13
US-09-798-889-164
; Sequence 164, Application US/09798889
; Publication No. US20030004324A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 31 Human secreted proteins
; FILE REFERENCE: PZ026P1
; CURRENT APPLICATION NUMBER: US/09/798,889
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/393,022
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,714
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,686
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,696
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 164
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-798-889-164

Query Match 70.6%; Score 36; DR 11; Length 195;
Best Local Similarity 66.7%; Pred. No. 11e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 9
| | | : | | | |
Db 103 KMLLELFCK 111

RESULT 14
US-09-764-868-1119
; Sequence 1119, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1119
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (187)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (191)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-1119

Query Match 68.6%; Score 35; DB 10; Length 197;
Best Local Similarity 75.0%; Pred. No. 1.6e-02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CLIQLFCK 9
 | | | | |
Db 95 CLINRECK 102

RESULT 15

US-09-764-868-1107
; Sequence 1107, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1107
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (216)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-1107

Query Match 68.6%; Score 35; DB 10; Length 228;
Best Local Similarity 75.0%; Pred. No. 1.9e-02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CLIQLFCK 9
 | | | | |
Db 44 CLINRECK 51

Search completed: October 14, 2003, 14:44:52
Job time : 22.9375 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 ; Search time 11.8125 Seconds
(without alignments)
73.271 Million cell updates/sec

Title: US-09-881-490-191
Perfect score: 51
Sequence: 1 KCLIQLFCK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 38 | 74.5 | 313 | 2 F45774 | odorant receptor 8 |
| 2 | 38 | 74.5 | 661 | 2 I52603 | MPS1 protein - mou |
| 3 | 37 | 72.5 | 163 | 2 F85046 | hypothetical prote |
| 4 | 37 | 72.5 | 259 | 2 P00687 | cyclin - anthracno |
| 5 | 36 | 70.6 | 257 | 2 E82871 | dimethyladenosine |
| 6 | 35 | 68.6 | 208 | 2 A41636 | GTP-binding protei |
| 7 | 35 | 68.6 | 319 | 2 T44833 | glycosyl transfera |
| 8 | 35 | 68.6 | 341 | 2 T25051 | hypothetical prote |
| 9 | 35 | 68.6 | 432 | 2 AF0567 | probable permease |
| 10 | 35 | 68.6 | 462 | 2 G96772 | hypothetical prote |
| 11 | 35 | 68.6 | 584 | 2 E71643 | poly-beta-hydroxyb |
| 12 | 35 | 68.6 | 973 | 2 H86428 | hypothetical prote |
| 13 | 35 | 68.6 | 5376 | 2 T42215 | zonadhesin - mouse |
| 14 | 34 | 66.7 | 265 | 2 T14645 | hypothetical prote |
| 15 | 34 | 66.7 | 635 | 2 T00011 | ccal protein - rat |
| 16 | 34 | 66.7 | 665 | 2 D96621 | auxin response fac |
| 17 | 34 | 66.7 | 846 | 2 JC7720 | acetyltransferase |
| 18 | 34 | 66.7 | 1142 | 2 T46155 | hypothetical prote |
| 19 | 34 | 66.7 | 1289 | 2 E90098 | RNA polymerase III |
| 20 | 34 | 66.7 | 2747 | 2 B49132 | fat facets (faf) s |
| 21 | 33.5 | 65.7 | 2471 | 2 T03820 | probable histidine |
| 22 | 33 | 64.7 | 126 | 2 T23246 | hypothetical prote |
| 23 | 33 | 64.7 | 127 | 2 E81134 | hypothetical prote |
| 24 | 33 | 64.7 | 175 | 2 T23245 | hypothetical prote |
| 25 | 33 | 64.7 | 340 | 2 T32104 | hypothetical prote |
| 26 | 33 | 64.7 | 381 | 1 A47327 | selenoprotein P pr |
| 27 | 33 | 64.7 | 504 | 2 T48992 | hypothetical prote |
| 28 | 33 | 64.7 | 522 | 2 A31556 | glucose transport |
| 29 | 33 | 64.7 | 523 | 2 S06920 | glucose transport |

| | | | | | |
|----|------|------|------|----------|--------------------|
| 30 | 33 | 64.7 | 577 | 2 T09024 | proline-rich prote |
| 31 | 33 | 64.7 | 645 | 2 F86627 | LysR family transc |
| 32 | 33 | 64.7 | 727 | 2 T25362 | hypothetical prote |
| 33 | 33 | 64.7 | 942 | 2 S49109 | spherulin - Melolo |
| 34 | 33 | 64.7 | 1084 | 1 S19661 | DNA-directed DNA p |
| 35 | 33 | 64.7 | 1086 | 2 T43266 | DNA-directed DNA p |
| 36 | 33 | 64.7 | 1320 | 2 S57113 | BUD4 protein - yea |
| 37 | 32.5 | 63.7 | 505 | 2 T28172 | hypothetical prote |
| 38 | 32.5 | 63.7 | 666 | 2 T03090 | hypothetical prote |
| 39 | 32 | 62.7 | 77 | 2 R82473 | hypothetical prote |
| 40 | 32 | 62.7 | 160 | 2 E71197 | hypothetical prote |
| 41 | 32 | 62.7 | 169 | 2 G72096 | hypothetical prote |
| 42 | 32 | 62.7 | 169 | 2 E86525 | hypothetical prote |
| 43 | 32 | 62.7 | 232 | 2 T20934 | hypothetical prote |
| 44 | 32 | 62.7 | 312 | 2 A86279 | F14L17.21 protein |
| 45 | 32 | 62.7 | 328 | 2 S73842 | thymidylate synth |

ALIGNMENTS

RESULT 1

E45774
odorant receptor 8 - channel catfish
C:Species: Ictalurus punctatus (channel catfish)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: E45774
R:Ngai, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.
Cell 72, 657-666, 1993
A:Title: The family of genes encoding odorant receptors in the channel catfish.
A:Reference number: A45774; MUID:93201590; PMID:7916654
A:Accession: E45774
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-313 <NGA>
A:Experimental source: olfactory epithelium
A>Note: sequence extracted from NCBI backbone (NCBIP:127748)
C:Superfamily: olfactory receptor OR14
C:Keywords: olfaction; transmembrane protein

Query Match 74.5%; Score 38; DB 2; Length 313;
Best Local Similarity 71.4%; Pred. No. 10;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CLIQLFC 8
Db 98 CLVQMFC 104

RESULT 2

I52603
MPS1 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: I52603
R:Spillsbury, K.; O'Mara, M.A.; Wu, W.M.; Rowe, P.B.; Symonds, G.; Takayama, Y.
Blood 85, 1620-1629, 1995
A:Title: Isolation of a novel macrophage-specific gene by differential cDNA analysis:
A:Reference number: I52603; MUID:95195232; PMID:7888681
A:Accession: I52603
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-661 <RES>
A:Cross-references: GB:L20315; NID:g431419; PIDN:AAA73957.1; PID:g431420

Query Match 74.5%; Score 38; DB 2; Length 661;
Best Local Similarity 55.6%; Pred. No. 19;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCLIQLFCK 9
Db 434 KCTLKIFCK 442

```
RESULT 3
F85046
hypothetical protein AT4g03680 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C:Accession: F85046
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: F85046
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-163 <STO>
A:Cross-references: GB:NC_001268; NID:g7270691; PIDN:CAB77653.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4g03680
A:Map position: 4

Query Match          72.5%; Score 37; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCLIQLF 7
    |||||
Db 7 KCLIQLF 13

RESULT 4
PN0687
cyclin - antheranose fungus (Colletotrichum gloeosporioides) (fragment)
C:Species: Glomerella cingulata, Colletotrichum gloeosporioides
C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 17-Mar-1999
C:Accession: PN0687
R:Masel, A.M.; Struijk, N.; McIntyre, C.L.; Irwin, J.A.G.; Manners, J.M.
Gene 133, 141-145, 1993
A:Title: A strain-specific cyclin homolog in the fungal phytopathogen Colletotrichum glo
A:Reference number: PN0687; MUID:94040789; PMID:8224886
A:Accession: PN0687
A:Molecule type: mRNA
A:Residues: 1-259 <MAS>
C:Superfamily: cyclin
F:48-193/Region: cyclin box

Query Match          72.5%; Score 37; DB 2; Length 259;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CLIQLFC 8
    |||||
Db 186 CFIQLFC 192

RESULT 5
E82871
dimethyladenosine transferase UU601 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: E82871
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A:Reference number: A82870
A:Accession: E82871
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <GLA>
A:Cross-references: GB:AE002158; GB:AF222894; NID:g6899599; PIDN:AAF31015.1; GSPDB:GN001
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: KsgA; UU601
A:Genetic code: SGC3
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```
C:Superfamily: rRNA (adenine-N6-)-methyltransferase

Query Match          70.6%; Score 36; DB 2; Length 257;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIQLFCK 9
    |||||
Db 152 LVQLFCK 158

RESULT 6
A41636
GTP-binding protein rah - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 02-Feb-2001
C:Accession: A41636
R:Morimoto, B.H.; Chuang, C.C.; Koshland Jr., D.E.
Genes Dev. 5, 2386-2391, 1991
A:Title: Molecular cloning of a member of a new class of low-molecular-weight GTP-bi
A:Reference number: A41636; MUID:92090719; PMID:1752434
A:Accession: A41636
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-208 <MOR>
A:Cross-references: GB:S72304; NID:g240985; PIDN:AAB20669.1; PID:g240986
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: membrane trafficking; nucleotide binding; P-loop
F:8-15/Region: nucleotide-binding motif A (P-loop)

Query Match          68.6%; Score 35; DB 2; Length 208;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CLIQLFCK 9
    |||||
Db 16 CLINRFCK 23

RESULT 7
T44833
glycosyl transferase homolog [imported] - Acinetobacter lwoffii
C:Species: Acinetobacter lwoffii
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 19-May-2000
C:Accession: T44833
R:Nakar, D.; Gutnick, D.L.
submitted to the EMBL Data Library, July 1999
A:Description: Genomic organization of the wce region of Acinetobacter lwoffii RAG-1
A:Reference number: Z22856
A:Accession: T44833
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-319 <NAK>
A:Cross-references: FMBL:AJ243431; PIDN:CABS7201.1
A:Experimental source: strain RAG-1
C:Genetics:
A:Gene: wceD
C:Superfamily: Acinetobacter lwoffii glycosyl transferase homolog

Query Match          68.6%; Score 35; DB 2; Length 319;
Best Local Similarity 62.5%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 CLIQLFCK 9
    |||||
Db 197 CLIDIFCE 204

RESULT 8
T25051
hypothetical protein T21B4.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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C;Accession: T25051
R;Smye, R.
Submitted to the EMBL Data Library, October 1996
A;Reference number: Z19974
A;Accession: T25051
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-341 <WIL>
A;Cross-references: EMBL:Z81124; PIDN:CA803372.1; GSPDB:GN00020; CESP:T21B4.6
A;Experimental source: clone T21B4
C;Genetics:
A;Gene: CESP:T21B4.6
A;Map position: 2
A;Introns: 120/1: 183/3
C;Superfamily: Caenorhabditis hypothetical protein C49G7.2

Query Match      68.6%; Score 35; DB 2; Length 341;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 KCLQLFCK 9
Db      316 KFLISLFC 324

RESULT 9
AF0567
probable permease protein STY0572 [imported] - Salmonella enterica subsp. enterica serov
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF0567
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF0567
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-432 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05008.1; PID:ql6501791; GSPDB:GN00176
C;Genetics:
A;Gene: STY0572

Query Match      68.6%; Score 35; DB 2; Length 432;
Best Local Similarity 71.4%; Pred. No. 49;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CLQLFCK 8
Db      57 CLVQAFCK 63

RESULT 10
G96772
hypothetical protein F1M20.8 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: G96772
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C-
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tal-
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: T25051
R;Smye, R.
Submitted to the EMBL Data Library, October 1996
A;Reference number: Z19974
A;Accession: T25051
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-341 <WIL>
A;Cross-references: EMBL:Z81124; PIDN:CA803372.1; GSPDB:GN00020; CESP:T21B4.6
A;Experimental source: clone T21B4
C;Genetics:
A;Gene: CESP:T21B4.6
A;Map position: 2
A;Introns: 120/1: 183/3
C;Superfamily: Caenorhabditis hypothetical protein C49G7.2

Query Match      68.6%; Score 35; DB 2; Length 341;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 KCLQLFCK 9
Db      316 KFLISLFC 324

RESULT 9
AF0567
probable permease protein STY0572 [imported] - Salmonella enterica subsp. enterica serov
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF0567
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF0567
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-432 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05008.1; PID:ql6501791; GSPDB:GN00176
C;Genetics:
A;Gene: STY0572

Query Match      68.6%; Score 35; DB 2; Length 432;
Best Local Similarity 71.4%; Pred. No. 49;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CLQLFCK 8
Db      57 CLVQAFCK 63

RESULT 10
G96772
hypothetical protein F1M20.8 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: G96772
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C-
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tal-
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: G96772
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-462 <STO>
A;Cross-references: GB:AE005173; NID:g6539242; PIDN:AAF15912.1; GSPDB:GN00141
C;Genetics:
A;Gene: F1M20.8
A;Map position: 1

Query Match      68.6%; Score 35; DB 2; Length 462;
Best Local Similarity 50.0%; Pred. No. 52;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CLQLFCK 9
Db      317 CMVDLFCR 324

RESULT 11
E71643
poly-beta-hydroxybutyrate polymerase (phbC2) RP820 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C;Accession: E71643
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmar
Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria
A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: E71643
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-584 <AND>
A;Cross-references: GB:AJ235273; GB:AJ235269; NID:g3861237; PIDN:CAA15245.1; PID:g38
A;Experimental source: strain Madrid E
C;Genetics:
A;Gene: phbC2; RP820
C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC

Query Match      68.6%; Score 35; DB 2; Length 584;
Best Local Similarity 62.5%; Pred. No. 62;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CLQLFCK 9
Db      51 CIIEQFCK 58

RESULT 12
H86428
hypothetical protein F26G16.3 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: H86428
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Al-
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Ki
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marz
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tal
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H86428
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-973 <STO>
A;Cross-references: GB:AE005172; NID:g6634764; PIDN:AAF19744.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

Query Match      68.6%; Score 35; DB 2; Length 973;
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Best Local Similarity 85.7%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CLIQIFC 8
Db 810 CKIQIFC 816

RESULT 13
T42215
zonadhesin - mouse
N:Alternate names: sperm-specific membrane protein
C:Species: Mus musculus (house mouse)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T42215
R:Gao, Z.; Garbers, D.L.
J. Biol. Chem. 273, 3415-3421, 1998
A:Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane protein
A:Reference number: Z22080; MUID:98123114; PMID:9452463
A:Accession: T42215
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-5376 <GAO>
A:Cross-references: EMBL:U97068; NID:g3327420; PID:g3327421; PIDN:AAC26680.1
C:Genetics:
A:Gene: Zan
A:Map position: 5
C:Function:
A:Description: functions in multiple cell adhesion processes
A:Note: found exclusively on the apical region of the sperm head
C:Keywords: cell adhesion

Query Match 68.6%; Score 35; DB 2; Length 5376;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLIQIFC 8
Db 3231 KCVLRIFC 3238

RESULT 14
T14645
hypothetical protein 265 - Sorghum mitochondrion
C:Species: mitochondrion Sorghum bicolor (sorghum)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: T14645
R:Tang, H.V.; Pring, D.R.; Muza, F.R.; Yan, B.
Curr. Genet. 29, 265-274, 1996
A:Title: Sorghum mitochondrial orf25 and a related chimeric configuration of a male-sterile
A:Reference number: S65767; MUID:96163056; PMID:8595673
A:Accession: T14645
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-265 <VAN>
A:Cross-references: EMBL:U22068; NID:g733079; PIDN:AAA97555.1; PID:g733080
A:Experimental source: strain IS112C; coleoptile
C:Genetics:
A:Genome: mitochondrion
C:Keywords: mitochondrion

Query Match 66.7%; Score 34; DB 2; Length 265;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CLIQIFC 8
Db 228 CLIQIFC 234

RESULT 15
T00011
ccal protein - rat

C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C:Accession: T00011
R:Hayashi, Y.; Kiyono, T.; Fujita, M.; Ishibashi, M.
J. Biol. Chem. 272, 18082-18086, 1997
A:Title: Ccal is required for formation of growth-arrested confluent monolayer of rat
A:Reference number: Z14036; MUID:97364729; PMID:9218439
A:Accession: T00011
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-635 <HAY>
A:Cross-references: EMBL:AB000215; NID:g2564000; PIDN:BAA22932.1; PID:g2564001
C:Genetics:
A:Gene: ccal
C:Superfamily: rat ccal protein

Query Match 66.7%; Score 34; DB 2; Length 635;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CLIQIFC 8
Db 53 CYLQIFC 59

Search completed: October 14, 2003, 14:38:08
Job time : 13.8125 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 ; Search time 6.375 Seconds
(without alignments)
66.391 Million cell updates/sec

Title: US-09-881-490-191
Perfect score: 51
Sequence: 1 KCLIQLFCK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs. 47026705 residues

Total number of hits satisfying chosen parameters: 227863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 39 | 76.5 | 886 | 1 VP39_HUMAN | Q96JC1 homo sapien |
| 2 | 39 | 76.5 | 886 | 1 VP39_MOUSE | Q8r5i3 mus musculu |
| 3 | 37 | 72.5 | 245 | 1 CGL_COIGI | Q06374 collectotric |
| 4 | 36 | 70.6 | 277 | 1 KSCA_UREPA | Q9ppn8 ureaplasma |
| 5 | 35 | 68.6 | 259 | 1 RB34_HUMAN | Q9bzq1 homo sapien |
| 6 | 35 | 68.6 | 259 | 1 RB34_MOUSE | Q64008 mus musculu |
| 7 | 35 | 68.6 | 5376 | 1 ZAN_MOUSE | Q88799 mus musculu |
| 8 | 34 | 66.7 | 318 | 1 OYD1_HUMAN | Q9h346 homo sapien |
| 9 | 34 | 66.7 | 2778 | 1 FAF_DROME | P55824 drosophila |
| 10 | 33 | 64.7 | 291 | 1 RT02_MOUSE | Q924t2 mus musculu |
| 11 | 33 | 64.7 | 315 | 1 OXM1_HUMAN | Q9h34t homo sapien |
| 12 | 33 | 64.7 | 381 | 1 SELP_HUMAN | P49908 homo sapien |
| 13 | 33 | 64.7 | 522 | 1 GTR2_RAT | P12336 rattus norv |
| 14 | 33 | 64.7 | 523 | 1 GTR2_MOUSE | P14246 mus musculu |
| 15 | 33 | 64.7 | 602 | 1 S21F_MACFA | Q9gmub macaca fasc |
| 16 | 33 | 64.7 | 712 | 1 S21F_HUMAN | Q9nyb5 homo sapien |
| 17 | 33 | 64.7 | 1447 | 1 BUD4_YEAST | P47136 saccharomyc |
| 18 | 32 | 62.7 | 416 | 1 TC10_HUMAN | Q12799 homo sapien |
| 19 | 32 | 62.7 | 497 | 1 ND2M_CHOCR | P48903 chondrus cr |
| 20 | 32 | 62.7 | 732 | 1 YLH3_SCHPO | Q9hgq3 schizosacch |
| 21 | 32 | 62.7 | 815 | 1 KINH_CAEEL | P34540 caenorhabdi |
| 22 | 32 | 62.7 | 947 | 1 PMA2_ARATH | P19456 arabidopsis |
| 23 | 32 | 62.7 | 948 | 1 PMA1_ARATH | P20649 arabidopsis |
| 24 | 32 | 62.7 | 960 | 1 CAP2_SORBI | P29194 sorghum bic |
| 25 | 32 | 62.7 | 967 | 1 CAP2_MAIZE | P51059 zea mays (m |
| 26 | 31 | 60.8 | 127 | 1 ATP2_PROMO | P29705 propionigen |
| 27 | 31 | 60.8 | 246 | 1 ENV_RSVSR | P03397 rous sarcom |
| 28 | 31 | 60.8 | 279 | 1 IACR_STAXY | O33813 staphylococ |
| 29 | 31 | 60.8 | 380 | 1 SELP_MOUSE | P70274 mus musculu |
| 30 | 31 | 60.8 | 385 | 1 SELP_RAT | P25236 rattus norv |
| 31 | 31 | 60.8 | 391 | 1 P53_RABIT | Q95330 oryctolagus |
| 32 | 31 | 60.8 | 438 | 1 RUMA_HAFIN | P44643 haemophilus |
| 33 | 31 | 60.8 | 480 | 1 YH9Q_YEAST | P36348 saccharomyc |

| | | | | | |
|----|------|------|------|--------------|--------------------|
| 34 | 31 | 60.8 | 503 | 1 C303_DROME | Q9v399 drosophila |
| 35 | 31 | 60.8 | 506 | 1 MURE_LEPIN | Q8f4j4 leptospira |
| 36 | 31 | 60.8 | 559 | 1 PAXI_CHICK | P49024 gallus gall |
| 37 | 31 | 60.8 | 591 | 1 PAXI_HUMAN | P49023 homo sapien |
| 38 | 31 | 60.8 | 993 | 1 DPOL_BPAPS | Q9tlq3 bacterioph |
| 39 | 31 | 60.8 | 998 | 1 GTFI_HUMAN | P78347 h general t |
| 40 | 31 | 60.8 | 998 | 1 GTFI_MOUSE | Q9esz8 mus musculu |
| 41 | 31 | 60.8 | 1318 | 1 YAB2_SCHPO | Q09804 schizosacch |
| 42 | 31 | 60.8 | 2670 | 1 YAQ5_SCHPO | Q10105 schizosacch |
| 43 | 30.5 | 59.8 | 685 | 1 CFAH_BOVIN | Q28085 bos taurus |
| 44 | 30 | 58.8 | 74 | 1 SSPS_STRPY | P29840 streptococc |
| 45 | 30 | 58.8 | 189 | 1 AP0D_HUMAN | P05090 homo sapien |

ALIGNMENTS

RESULT 1
VP39_HUMAN
ID VP39_HUMAN STANDARD; PRT; 886 AA.
AC Q96JCI; Q94869; Q96B93; Q96RM0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vam6/Vps39-like protein (hVam6p).
CN VPS39 OR KIAA0770.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=21342080; PubMed=11448994;
RA Caplan S., Hartnell L.M., Aguilar R.C., Naslavsky N., Bonifacino J.S.;
RT "Human Vam6p promotes lysosome clustering and fusion in vivo.";
RL J. Cell Biol. 154:109-122(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=99087487; PubMed=9872452;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XI.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:277-286(1998).
RN [3]
RP SEQUENCE OF 98-886 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May play a role in clustering and fusion of late
CC endosomes and lysosomes.

CC -!- SUBUNIT: Homooligomer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and associated with the
CC membranes of lysosomes and late endosomes.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms-2;
CC Name=1;
CC IsoId=Q96JCL1-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q96JCL1-2; Sequence=VSP_004075;
CC -!- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in heart,
CC skeletal muscle, kidney, pancreas, brain, placenta and lung.
CC -!- SIMILARITY: Contains 1 CNH domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF280814; AAK72222.1; -;
CC EMBL; AF334400; AAK58862.1; -;
CC EMBL; AB018313; BAA34490.2; ALT_INIT.
CC EMBL; BC015817; AAL15817.1; ALT_INIT.
CC InterPro; IPR001180; Citron.
CC Pfam; PF00780; CNH; 1.
CC KW Transport; Protein transport; Alternative splicing.
CC FT DOMAIN 15 294 CNH.
CC FT VARSPLIC 47 58 VPADVASPEGS -> G (in isoform 2).
CC FT CONFLICT 98 100 YVH -> GTR (IN REF. 3).
CC FT CONFLICT 135 135 Q -> R (IN REF. 1; AF280814 AND 2).
CC SQ SEQUENCE 886 AA; 101780 MW; 2C0C48753AFB6A7F CRC64;
Query Match 76.5%; Score 39; DB 1; Length 886;
Best Local Similarity 75.0%; Pred. No. 8.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 CLIQLFCK 9
Db 621 CLIQLYCE 628
RESULT 2
VP39_MOUSE;
ID VP39_MOUSE STANDARD; PRI: 886 AA.
AC Q8R5L3; Q92213;
DI 28-FEB-2003 (Rel. 41, Created)
DI 28-FEB-2003 (Rel. 41, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vam6/Vps39-like protein (Vps39 protein).
GN VPS39 OR PLDN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=Swiss Webster / NIH;
RA Falcon-Perez J.M., Dell'Angelica E.C.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May play a role in clustering and fusion of late
CC endosomes and lysosomes (By similarity).
CC -!- SUBUNIT: Homooligomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and associated with the
CC membranes of lysosomes and late endosomes (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms-2;
CC Name=1;
CC IsoId=Q8R5L3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8R5L3-2; Sequence=VSP_004076;
CC -!- SIMILARITY: Contains 1 CNH domain.
CC -----
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CC -----
CC EMBL; AF281050; AAL79766.1; -;
CC EMBL; AF281051; AAL79767.1; -;
CC EMBL; BC007479; AAL79767.1; -;
CC MGD; MGI:1927580; Pldn.
CC GO; GO:0005768; C:endosome; IDA.
CC CO; GO:0006944; P:membrane fusion; IPI.
CC InterPro; IPR001180; Citron.
CC Pfam; PF00780; CNH; 1.
CC KW Transport; Protein transport; Alternative splicing.
CC FT DOMAIN 15 294 CNH.
CC FT VARSPLIC 47 58 VPADVASPEGS -> G (in isoform 2).
CC FT SEQUENCE 886 AA; 101692 MW; BD46EF52D404C2DA CRC64;
Query Match 76.5%; Score 39; DB 1; Length 886;
Best Local Similarity 75.0%; Pred. No. 8.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 CLIQLFCK 9
Db 621 CLIQLYCE 628
RESULT 3
CGI_COLGL
ID CGI_COLGL STANDARD; PRI: 245 AA.
AC Q06374;
DI 01-FEB-1995 (Rel. 31, Created)
DI 01-FEB-1995 (Rel. 31, Last sequence update)
DI 01-FEB-1995 (Rel. 31, Last annotation update)
DE Putative G1/S-specific cyclin.
GN CYCL.
OS Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella
OS cingulata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC Glomerella.
OX NCBI_TaxID=5457;
RN [1]

```
RP SEQUENCE FROM N.A.
RC STRAIN-Biotype B / Isolate race-3;
RX MEDLINE-94040789; PubMed-8224888;
RA Masel A.M., Struijk N., McIntyre C.L., Irwin J.A.G., Manners J.M.;
RT "A strain-specific cyclin homolog in the fungal phytopathogen
RT Colletotrichum gloeosporioides.";
RL Gene 133:141-145(1993).
CC -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
CC (START) TRANSITION. INTERACTS WITH THE CDC2 PROTEIN KINASE TO
CC FORM MPF (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. STRONGEST TO OTHER
CC G1/S CYCLINS.
CC -----
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CC -----
CC EMBL; X69099; CAA48845.1; --
CC InterPro; IPR006670; Cyclin.
CC InterPro; IPR006671; Cyclin_N.
CC Pfam; PF00134; cyclin; 1.
CC SMART; SM00385; CYCLIN; 1.
CC PROSITE; PS00292; CYCLINS; 1.
KW Cyclin; Cell cycle; Cell division.
SQ SEQUENCE 245 AA; 28143 MW; 587FE836383F5390 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 245;
Best Local Similarity 85.7%; Pred. No. 5.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CLIQFPC 8
DB 172 CFIQFPC 178

RESULT 4
KSGA_UREPA
ID KSGA_UREPA STANDARD; PRT; 277 AA.
AC Q9PPN8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, last sequence update)
DI 28-FEB-2003 (Rel. 41, last annotation update)
DE Dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6-N',
DE N'-adenosyl(rRNA) dimethyltransferase) (16S rRNA dimethylase) (High
DE level kasugamycin resistance protein ksgA) (Kasugamycin
DE dimethyltransferase).
GN KSGA OR UU601.
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID-134821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Serovar 3;
RX MEDLINE-20500219; PubMed-11048724;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
RT urealyticum.";
RL Nature 407:757-762(2000).
CC -!- FUNCTION: Specifically dimethylates two adjacent adenosines in the
CC loop of a conserved hairpin near the 3' end of 16S rRNA in the 30S
CC particle. Its inactivation leads to kasugamycin resistance (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE RRNA ADENINE N-6-METHYLTRANSFERASE
CC FAMILY. KSGA SUBFAMILY.
CC -----
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CC -----
CC EMBL; AE002158; AAF31015.1; ALT_INIT.
CC HSP; P13956; IQAM.
CC HAMAP; MF_00607; --; 1.
CC InterPro; IPR001737; RRNA_A_dimeth.
CC InterPro; IPR000051; SAM_bind.
CC Pfam; PF00398; RrnaAD; 1.
CC SMART; SM00650; RADc; 1.
CC TIGRFAMs; TIGR00755; ksgA; 1.
CC PROSITE; PS01131; RRNA_A_DIMETH; 1.
KW mRNA processing; Transferase; Methyltransferase;
KW Antibiotic resistance; Complete proteome.
SQ SEQUENCE 277 AA; 32145 MW; EC4E13D6B1549BCE CRC64;

Query Match 70.6%; Score 36; DB 1; Length 277;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIQLFCK 9
DB 172 LVQLFCK 178

RESULT 5
RB34_HUMAN
ID RB34_HUMAN STANDARD; PRT; 259 AA.
AC Q9B2G1; Q8NCJ8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, last sequence update)
DI 28-FEB-2003 (Rel. 41, last annotation update)
DE Ras-related protein Rab-34 (Rab-39) (Ras-related protein Rah).
GN RAB34 OR RAB39 OR RAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hong W.;
RT "Human Rab39 coding region (cDNA).";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Skeletal muscle;
RA Stanchi F., Lanfranchi G.;
RT "Full-length sequencing of 100 cDNA clones from human adult skeletal
RT muscle.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Embryo, and Mammary gland;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
CC TRAFFIC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAB FAMILY.
CC -----
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CC -----
DR EMBL; AF322067; AAK09397.1; -.
DR EMBL; AJ277106; CAC81760.1; -.
DR EMBL; AK027312; BAH55034.1; -.
DR EMBL; AK074689; BAC11141.1; -.
DR HSSP; PL7080; 1A2K.
DR Genew; HGNC:16519; RAB34.
DR InterPro; IPR003579; GTPase_Rab.
DR InterPro; IPR001806; Ras_trnsfrmng.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00071; ras; 1.
DR PRINTS; PR00449; RASTRNSFRMNG.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
KW GTP-binding; Lipoprotein; Prenylation; Transport; Protein transport;
KW Golgi stack; Polymorphism.
FT NP_BIND 59 66 GTP (BY SIMILARITY).
FT NP_BIND 107 111 GTP (BY SIMILARITY).
FT NP_BIND 166 169 GTP (BY SIMILARITY).
FT DOMAIN 81 89 EFFECTOR REGION (BY SIMILARITY).
FT LIPID 257 257 GERANYL-GERANYL (POTENTIAL).
FT LIPID 258 258 GERANYL-GERANYL (POTENTIAL).
FT VARIANT 197 197 V -> L (in dbSNP:12125).
FT FTID=VAR_015097.
FT CONFLICT 55 55 V -> I (IN REF. 3; BAC11141).
FT SEQUENCE 259 AA; 29044 MW; 6D38A6F090F9802D CRC64;
SQ
Query Match 68.6%; Score 35; DB 1; Length 259;
Best Local Similarity 75.0%; Pred. NO. 15;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CLIQLECK 9
DB 67 CLINRECK 74
RESULT 6
RB34_MOUSE STANDARD; PRT; 259 AA.
ID RB34_MOUSE Q99P59; Q99P90;
AC Q64008; Q99P59; Q99P90;
DT 30-MAY-2000 (Rel. 39, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ras-related protein Rab-34 (Rab-39) (Ras-related protein Rah) (Ras-
DE related homolog).
CN RAB34 OR RAB39 OR RAH1 OR RAH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Hong W.;
RT "Mouse Rab39 coding region (cDNA).";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Neuron;
RA Hari M., Morimoto B.H., Asai D.J.;
RT "Full length sequence of Rah, a novel member of the Rab family of
RT small GTPases.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 52-259 FROM N.A.
RC TISSUE=Neuron;
RX MEDLINE=92090719; PubMed=1752434;
RA Morimoto B.H., Chuang C.-C., Koshland D.E. Jr.;
RT "Molecular cloning of a member of a new class of low-molecular-weight
RT GTP-binding proteins.";
RL Genes Dev. 5:2386-2391(1991).
```

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CC -----
CC FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
CC TRAFFIC (BY SIMILARITY).
CC SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAB FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF322068; AAK09398.1; -.
DR EMBL; AF327929; AAK11241.1; -.
DR EMBL; S72304; AAB20669.1; -.
DR PIR; A41636; A41636.
DR HSSP; P06749; 1A2B.
DR MGD; MGI:104606; Rab34.
DR InterPro; IPR003579; GTPase_Rab.
DR InterPro; IPR001806; Ras_trnsfrmng.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00071; ras; 1.
DR PRINTS; PR00449; RASTRNSFRMNG.
DR SMART; SM00175; RAB; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
KW GTP-binding; Lipoprotein; Prenylation; Transport; Protein transport;
KW Golgi stack.
FT NP_BIND 59 66 GTP (BY SIMILARITY).
FT NP_BIND 107 111 GTP (BY SIMILARITY).
FT NP_BIND 166 169 GTP (BY SIMILARITY).
FT DOMAIN 81 89 EFFECTOR REGION (BY SIMILARITY).
FT LIPID 257 257 GERANYL-GERANYL (POTENTIAL).
FT LIPID 258 258 GERANYL-GERANYL (POTENTIAL).
FT CONFLICT 52 52 I -> N (IN REF. 3).
FT SEQUENCE 259 AA; 29100 MW; 158F5132F0DDE808 CRC64;
SQ
Query Match 68.6%; Score 35; DB 1; Length 259;
Best Local Similarity 75.0%; Pred. NO. 15;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CLIQLECK 9
DB 67 CLINRECK 74
RESULT 7
ZAN_MOUSE STANDARD; PRT; 5376 AA.
ID ZAN_MOUSE O08647;
AC O88799; O08647;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Zonadhesin precursor.
GN ZAN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=98123114; PubMed=9452463;
RA Gao Z., Garbers D.L.;
RT "Species diversity in the structure of zonadhesin, a sperm-specific
RT membrane protein containing multiple cell adhesion molecule-like
RT domains.";
RL J. Biol. Chem. 273:3415-3421(1998).
RN [2]
RP SEQUENCE OF 4864-5376 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=97271566; PubMed=9126492;
RA Gao Z., Harumi T., Garbers D.L.;
RT "Chromosome localization of the mouse zonadhesin gene and the human
```



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RT zonadhesin gene (ZAN).";
RL Genomics 41:119-122(1997).
CC -!- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
CC OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
CC SIGNALING.
CC -!- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE
CC APICAL REGION OF THE SPERM HEAD.
CC -!- TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS.
CC -!- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATES SPERM ADHESION TO THE
CC ZONA PELLUCIDA.
CC -!- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
CC THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF
CC SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
CC -!- DOMAIN: THE VWFD DOMAIN 2 MAY MEDIATE COVALENT
CC OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
CC -!- SIMILARITY: Contains 3 MAM domains.
CC -!- SIMILARITY: Contains 25 VWFD domains.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -----
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CC -----
DR EMBL; U97068; AAC26680.1; -.
DR EMBL; U83190; AAC53125.1; -.
DR PIR; T42215; T42215.
DR MGD; MGI:106656; ZAN.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000998; MAM_domain.
DR InterPro; IPR002919; TIL_Cysrich.
DR InterPro; IPR003328; TILa_Cysrich.
DR InterPro; IPR001007; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF00629; MAM; 3.
DR Pfam; PF01826; TIL; 25.
DR Pfam; PF02345; TILa; 25.
DR Pfam; PF00094; vwd; 4.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00274; FOLN; 11.
DR SMART; SM00137; MAM; 2.
DR SMART; SM00214; VWC; 17.
DR SMART; SM00216; VWD; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 18.
DR PROSITE; PS00740; MAM_1; FALSE_NEG.
DR PROSITE; PS50060; MAM_2; 3.
KW Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
KW Repeat.
FT SIGNAL 1 17 POTENTIAL..
FT CHAIN 18 5376 ZONADHESIN.
FT DOMAIN 18 5310 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 5311 5337 POTENTIAL.
FT DOMAIN 5338 5376 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 45 210 MAM 1.
FT DOMAIN 215 374 MAM 2.
FT DOMAIN 377 542 MAM 3.
FT DOMAIN 547 1170 80 X HEPTAPEPTIDE REPEATS (APPROXIMATE)
(MUCIN-LIKE DOMAIN).
FT DOMAIN 1171 1280 VWFD 1 (PARTIAL).
FT DOMAIN 1281 1669 VWFD 2.
FT DOMAIN 1670 2056 VWFD 3.
FT DOMAIN 2057 2459 VWFD 4.
FT DOMAIN 2460 2579 VWFD 5 (PARTIAL).
FT DOMAIN 2580 2699 VWFD 6 (PARTIAL).
FT DOMAIN 2700 2819 VWFD 7 (PARTIAL).
FT DOMAIN 2820 2939 VWFD 8 (PARTIAL).
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FT DOMAIN 2940 3059 VWFD 9 (PARTIAL).
FT DOMAIN 3060 3179 VWFD 10 (PARTIAL).
FT DOMAIN 3180 3299 VWFD 11 (PARTIAL).
FT DOMAIN 3300 3416 VWFD 12 (PARTIAL).
FT DOMAIN 3417 3536 VWFD 13 (PARTIAL).
FT DOMAIN 3537 3656 VWFD 14 (PARTIAL).
FT DOMAIN 3657 3776 VWFD 15 (PARTIAL).
FT DOMAIN 3777 3892 VWFD 16 (PARTIAL).
FT DOMAIN 3893 4028 VWFD 17 (PARTIAL).
FT DOMAIN 4029 4148 VWFD 18 (PARTIAL).
FT DOMAIN 4149 4263 VWFD 19 (PARTIAL).
FT DOMAIN 4264 4383 VWFD 20 (PARTIAL).
FT DOMAIN 4384 4503 VWFD 21 (PARTIAL).
FT DOMAIN 4504 4623 VWFD 22 (PARTIAL).
FT DOMAIN 4624 4743 VWFD 23 (PARTIAL).
FT DOMAIN 4744 4863 VWFD 24 (PARTIAL).
FT DOMAIN 4864 5261 VWFD 25.
FT DOMAIN 5259 5295 EGF-LIKE.
FT DISULFID 5263 5274 BY SIMILARITY.
FT DISULFID 5268 5283 BY SIMILARITY.
FT DISULFID 5285 5294 BY SIMILARITY.
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1216 1216 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1239 1239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1314 1314 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1814 1814 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1908 1908 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1933 1933 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2028 2028 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2111 2111 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2142 2142 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2332 2332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2533 2533 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2575 2575 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2692 2692 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2812 2812 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3052 3052 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3065 3065 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3144 3144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3172 3172 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3288 3288 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3292 3292 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3782 3782 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4005 4005 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4136 4136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4243 4243 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4254 4254 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4335 4335 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4376 4376 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4586 4586 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 5136 5136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 5252 5252 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 5376 AA; 579908 MW; 0E44DB77DF2A2620 CRC64;
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Query Match 68.6%; Score 35; DB 1; Length 5376;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;

Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KCLIQLCF 8

II:::II

Db 3231 KCVLRIFC 3238

RESULT 8

OYD1_HUMAN

ID OYD1_HUMAN STANDARD; PRT; 318 AA.

AC Q9H346;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Olfactory receptor 52D1 (HORS'beta14).

GN OR52D1.

OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20570519; PubMed=11121057;
RA Bulger M., Bender M.A., van Doorninck J.H., Wertman B., Farrell C.M.,
RA Felsenfeld G., Groudine M., Hardison R.;
RT "Comparative structural and functional analysis of the olfactory
RT receptor genes flanking the human and mouse beta-globin gene
RT clusters.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).
CC -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: AF137396; AAG41676.1; -
DR GO: GO:0016021; C: integral to membrane; NAS.
DR GO: GO:0004984; F: olfactory receptor activity; NAS.
DR GO: GO:0007608; P: olfaction; NAS.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 29 52 1 (POTENTIAL).
FT DOMAIN 53 60 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 61 82 2 (POTENTIAL).
FT DOMAIN 83 103 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 104 123 3 (POTENTIAL).
FT DOMAIN 124 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 161 4 (POTENTIAL).
FT DOMAIN 162 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 222 5 (POTENTIAL).
FT DOMAIN 223 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 262 6 (POTENTIAL).
FT DOMAIN 263 278 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 279 298 7 (POTENTIAL).
FT DOMAIN 299 318 CYTOPLASMIC (POTENTIAL).
FT DISULFID 100 192 HY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 318 AA; 35121 MW; 178968087D613CB2 CRC64;

Query Match 66.7%; Score 34; DB 1; Length 318;
Best Local Similarity 71.4%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CLIQLEFC 8
Db 100 CLAQMFC 106

RESULT 9
FAF_DROME STANDARD; PRT: 2778 AA.
ID FAF_DROME Q9V9T6; Q9Y027;
AC P55824; Q9V9T6; Q9Y027;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable ubiquitin carboxyl-terminal hydrolase FAF (EC 3.1.2.15)
DE (Ubiquitin thiolesterase FAF) (Ubiquitin-specific processing protease

DE FAF) (Deubiquitinating enzyme FAF) (Fat facets protein).
GN FAF OR BCDNA:LD22582 OR CG1945.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND TISSUE SPECIFICITY.
RC TISSUE=Eye imaginal disk;
RX MEDLINE=93202020; PubMed=1295747;
RA Fischer-Vize J.A., Rubin G.M., Lehmann R.;
RT "The fat facets gene is required for Drosophila eye and embryo
RT development.";
RL Development 116:985-1000(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Heeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Heinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP REVISIONS, AND ALTERNATIVE SPLICING.
RC STRAIN=Berkeley;
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [4]
RP SEQUENCE OF 1089-2778 FROM N.A. (ISOFORM 1).

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RC STRAIN=Berkley;
RX MEDLINE=20196012; PubMed=10731138;
RA Rubin G.M., Hong L., Brokstein P., Evans-Holt M., Frise E.,
RA Stapleton M., Harvey D.A.;
RT "A Drosophila complementary DNA resource.";
RL Science 287:2222-2224(2000).
CC -!- FUNCTION: REQUIRED FOR EYE AND EMBRYO DEVELOPMENT, AND PLAYS A
CC ROLE IN COMPOUND EYE ASSEMBLY AND OOGENESIS RESPECTIVELY. IN THE
CC LARVAL EYE DISKS, CELLS OUTSIDE THE ASSEMBLING FACETS REQUIRE TH-S
CC PROTEIN FOR SHORT-RANGE CELL INTERACTIONS THAT PREVENT THE MYSTERY
CC CELLS FROM BECOMING PHOTORECEPTORS. IT IS ALSO REQUIRED FOR
CC NUCLEAR MIGRATION AND CELLULARIZATION IN EARLY EMBRYOGENESIS AND
CC COULD PLAY A ROLE IN POLE CELL DETERMINATION, DEVELOPMENT OR
CC FUNCTION.
CC -!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O -
CC ubiquitin + a thiol.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms-3:
CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC Name=1;
CC IsoId=P55824-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P55824-2; Sequence=VSP_005270;
CC Name=3;
CC IsoId=P55824-3; Sequence=VSP_005269;
CC -!- TISSUE SPECIFICITY: EYE DISKS AND OVARIES.
CC -!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
CC -!- SIMILARITY: Belongs to peptidase family C19.
CC -----
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CC -----
CC EMBL; L04959; AAF01345.1; -.
CC EMBL; L04958; AAF01346.1; -.
CC EMBL; L04960; AAF01347.1; -.
CC EMBL; L04960; AAF01348.1; -.
CC EMBL; AE003779; AAF57198.1; -.
CC EMBL; AE003779; AAN14291.1; -.
CC EMBL; AF145677; AAD38652.1; -.
CC MEROPS; C19.007; -.
CC FlyBase; FBgn0005632; faf.
CC GO; GO:0005737; C:cytoplasm; IDA.
CC GO; GO:0007349; P:cellularization; IMP.
CC GO; GO:0009795; P:embryonic morphogenesis; IMP.
CC GO; GO:0008583; P:mystery cell fate differentiation (sensu Dr. . .; IMP.
CC GO; GO:0007097; P:nuclear migration; IMP.
CC GO; GO:0006512; P:ubiquitin cycle; IGI.
CC InterPro; IPR001394; UCH-2.
CC Pfam; PF00443; UCH; 1.
CC PROSITE; PS00972; UCH_2_1; 1.
CC PROSITE; PS00973; UCH_2_2; 1.
CC PROSITE; PS50235; UCH_2_3; 1.
CC Ubl conjugation pathway; Hydrolase; Thiol protease;
KW Developmental protein; Vision; Alternative splicing.
FT ACT_SITE 1677 1677 BY SIMILARITY.
FT ACT_SITE 1978 1978 BY SIMILARITY.
FT ACT_SITE 1986 1986 BY SIMILARITY.
FT ACT_SITE 1986 1986 BY SIMILARITY.
FT ACT_SITE 2705 2778 KRRVILKKLVESKDEEDATTATTATTTEVTITSPATAIATA
FT VARSPLIC 2705 2778 ATLEPAGMSELTITMVEKNLIISQENPQAKSSIQ ->
FT VARSPLIC 2742 2778 NVV (in isoform 3).
FT VARSPLIC 2742 2778 /FTId-VSP_005269.
FT VARSPLIC 2742 2778 IATAATLEPAGMSELTITMVEKNLIISQENPQAKSSIQ ->
FT VARSPLIC 2742 2778 SQRQL (in isoform 2).
FT VARSPLIC 2742 2778 /FTId-VSP_005270.
FT CONFLICT 234 234 E -> D (IN REF. 1).
FT CONFLICT 2725 2725 T -> S (IN REF. 1; AAF01345).
FT CONFLICT 2725 2725 T -> S (IN REF. 1; AAF01345).
FT SEQUENCE 2778 AA: 311139 MW: FFB90438BA53A02B CRC64;
```

```
Query Match 66.7%; Score 34; DB 1; Length 2778;
Best Local Similarity 77.8%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 9
Db 2480 KCLTQLFHK 2488
      ||| ||| |
      ||| ||| |

RESULT 10
RT02_MOUSE
ID RT02_MOUSE STANDARD; PRT; 291 AA.
AC Q924T2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S2 (MRP-S2).
GN MRPS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21413863; PubMed=11402041;
RA Suzuki T., Terasaki M., Takemoto-Hori C., Hanada T., Ueda T., Wada A.,
RA Watanabe K.;
RT "Proteomic analysis of the mammalian mitochondrial ribosome.
RT Identification of protein components in the 28 S small subunit.";
RJ J. Biol. Chem. 276:33181-33195(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
CC EMBL; AB055389; BAB62530.1; -.
CC MGD; MGI:2153089; Mrps2.
CC InterPro; IPR001865; Ribosomal_S2.
CC InterPro; IPR005706; S2_bact_org.
CC Pfam; PF00318; Ribosomal_S2; 1.
CC PRINTS; PR00395; RIBOSOMALS2.
CC TIGRFAMS; TIGR01011; rpsB_bact; 1.
CC PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
KW Ribosomal protein; Mitochondrion.
SQ SEQUENCE 291 AA; 32313 MW; 33CFE4731BCEBADD CRC64;

Query Match 64.7%; Score 33; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IQLFCK 9
Db 243 IQLFCK 248
      |||||
      |||||

RESULT 11
OXM1_HUMAN
ID OXM1_HUMAN STANDARD; PRT; 315 AA.
AC Q9H341;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Olfactory receptor 51M1 (HORS'beta7).
GN OR51M1.
```

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20570519; PubMed=11121057;
RA Bulger M., Bender M.A., van Doorninck J.H., Wertman B., Farrell C.M.,
RA Felsenfeld G., Groudine M., Hardison R.;
RT "Comparative structural and functional analysis of the olfactory
RT receptor genes flanking the human and mouse beta-globin gene
RT clusters.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).
CC -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; AF137396; AAG41681.1; ALT_INIT.
DR GO; GO:0016021; C: integral to membrane; NAS.
DR GO; GO:0004984; F: olfactory receptor activity; NAS.
DR GO; GO:0007608; P: olfaction; NAS.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7Tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 26 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 27 50 1 (POTENTIAL).
FT DOMAIN 51 58 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 59 80 2 (POTENTIAL).
FT DOMAIN 81 101 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 102 121 3 (POTENTIAL).
FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 141 159 4 (POTENTIAL).
FT DOMAIN 160 196 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 197 220 5 (POTENTIAL).
FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 238 260 6 (POTENTIAL).
FT DOMAIN 261 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 295 7 (POTENTIAL).
FT DOMAIN 296 315 CYTOPLASMIC (POTENTIAL).
FT DISULFID 98 190 HY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 315 AA; 35462 MW; DC19D2F5456D2005 CRC64;

Query Match 64.7%; Score 33; DB 1; Length 315;
Best Local Similarity 71.4%; Pred. NO. 41;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CLIQLEFC 8
Db 98 CQIQMFC 104

RESULT 12
SELP_HUMAN
ID SELP_HUMAN STANDARD; PRI: 381 AA.
AC P49908;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Selenoprotein P precursor (Sep).
GN SEPP1 OR SELP.
```

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Heart, and Liver;
RX MEDLINE=93133023; PubMed=8421687;
RA Hill K.E., Lloyd R.S., Burk R.F.;
RT "Conserved nucleotide sequences in the open reading frame and 3'
RT untranslated region of selenoprotein P mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:537-541(1993).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE=94191007; PubMed=8142465;
RA Akesson B., Bellew T., Burk R.F.;
RT "Purification of selenoprotein P from human plasma.";
RL Biochim. Biophys. Acta 1204:243-249(1994).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=98413836; PubMed=9735174;
RA Mostert V., Lombeck I., Abel J.;
RT "A novel method for the purification of selenoprotein P from human
RT plasma.";
RL Arch. Biochem. Biophys. 357:326-330(1998).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=20239644; PubMed=10775431;
RA Mostert V.;
RT "Selenoprotein P: properties, functions, and regulation.";
RL Arch. Biochem. Biophys. 376:433-438(2000).
RN [5]
RP REVIEW.
RX MEDLINE=95017128; PubMed=7931697;
RA Burk R.F., Hill K.E.;
RT "Selenoprotein P. A selenium-rich extracellular glycoprotein.";
RL J. Nutr. 124:1891-1897(1994).
CC -!- FUNCTION: MIGHT BE RESPONSIBLE FOR SOME OF THE EXTRACELLULAR
CC ANTIOXIDANT DEFENSE PROPERTIES OF SELENIUM OR MIGHT BE INVOLVED IN
CC THE TRANSPORT OF SELENIUM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER AND HEART AND SECRETED INTO
CC THE PLASMA. IT IS ALSO FOUND IN THE KIDNEY.
CC -!- MISCELLANEOUS: THE SELENOCYSTEINES ARE ALL ENCODED BY THE OPAL
CC CODON, UGA.
CC -----
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CC -----
DR EMBL; Z11793; CAA77836.1; -.
DR PIR; A47327; A47327.
DR Genew; HGNC:10751; SEPP1.
DR MIM; 601484; -.
DR GO; GO:0008430; F: selenium binding activity; TAS.
DR GO; GO:0006979; P: response to oxidative stress; TAS.
DR Pfam; PF04593; Selp_C; 1.
DR Pfam; PF04592; Selp_N; 1.
KW Glycoprotein; Signal; Selenium; Selenocysteine; Plasma.
FT SIGNAL 1 19
FT CHAIN 20 381 SELENOPROTEIN P.
FT DOMAIN 244 249 POLY-HIS.
FT SE_CYS 59 59
FT SE_CYS 300 300
FT SE_CYS 318 318
FT SE_CYS 330 330
FT SE_CYS 345 345
FT SE_CYS 352 352
FT SE_CYS 367 367
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FT SE_CYS 369 369
FT SE_CYS 376 376
FT SE_CYS 378 378
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 381 AA; 42705 MW; 1A82FFA0BCD13CD7 CRC64;

Query Match 64.7%; Score 33; DB 1; Length 381;
Best Local Similarity 55.6%; Pred. No. 50;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KCLIQLECK 9
DB 280 RCINQLLCK 288

RESULT 13
GTR2_RAT STANDARD; PRT; 522 AA.
ID GTR2_RAT
AC P12336;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Solute carrier family 2, facilitated glucose transporter, member 2
DE (Glucose transporter type 2, liver).
GN SLC2A2 OR GLUT2 OR GLUT-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=89003066; PubMed=3048704;
RA Thorens B., Sarkar H.K., Kaback H.R., Lodish H.F.;
RT "Cloning and functional expression in bacteria of a novel glucose
RT transporter present in liver, intestine, kidney, and beta-pancreatic
RT islet cells.";
RL Cell 55:281-290(1988).
CC -1- FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. THIS ISOFORM LIKELY
CC MEDIATES THE BIDIRECTIONAL TRANSFER OF GLUCOSE ACROSS THE PLASMA
CC MEMBRANE OF HEPATOCYTES AND IS RESPONSIBLE FOR UPTAKE OF GLUCOSE
CC BY THE BETA CELLS; MAY COMPRISE PART OF THE GLUCOSE-SENSING
CC MECHANISM OF THE BETA CELL. MAY ALSO PARTICIPATE WITH THE
CC NA(+)/GLUCOSE COTRANSPORTER IN THE TRANSCYTOPLASMIC TRANSPORT OF
CC GLUCOSE IN THE SMALL INTESTINE AND KIDNEY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: PRESENT IN LIVER, INTESTINE, KIDNEY AND
CC BETA-PANCREATIC ISLET CELLS.
CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
CC TRANSPORTER SUBFAMILY.
CC -----
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CC -----
CC EMBL; J03145; AAA41298.1; -.
CC PIR; A31556; A31556.
CC InterPro; IPR007114; MFS.
CC InterPro; IPR005828; Sub_transporter.
CC InterPro; IPR005829; Sug_transporter.
CC InterPro; IPR003663; Sugar_transpt.
CC Pfam; PF00083; sugar_tr; 1.
CC PRINTS; PR00171; SUGRTRNSPORT.
CC TIGRFAMs; TIGR00879; SP; 1.
CC PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
```

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DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
KW Transmembrane; Sugar transport; Transport; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 1 (POTENTIAL).
FT DOMAIN 32 96 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 97 117 2 (POTENTIAL).
FT DOMAIN 118 125 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 126 146 3 (POTENTIAL).
FT DOMAIN 147 156 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 157 177 4 (POTENTIAL).
FT DOMAIN 178 185 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 186 206 5 (POTENTIAL).
FT DOMAIN 207 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 236 6 (POTENTIAL).
FT DOMAIN 237 301 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 302 322 7 (POTENTIAL).
FT DOMAIN 323 337 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 338 358 8 (POTENTIAL).
FT DOMAIN 359 365 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 366 386 9 (POTENTIAL).
FT DOMAIN 387 401 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 402 422 10 (POTENTIAL).
FT DOMAIN 423 431 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 432 452 11 (POTENTIAL).
FT DOMAIN 453 459 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 460 480 12 (POTENTIAL).
FT DOMAIN 481 522 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 522 AA; 57085 MW; 075AB81E56CF33F7 CRC64;

Query Match 64.7%; Score 33; DB 1; Length 522;
Best Local Similarity 62.5%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCLIQLEFC 8
DB 230 QCLLLFLFC 237

RESULT 14
GTR2_MOUSE STANDARD; PRT; 523 AA.
ID GTR2_MOUSE
AC P14246; Q9DBA7;
DT 01-JAN-1990 (Rel. 13, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Solute carrier family 2, facilitated glucose transporter, member 2
DE (Glucose transporter type 2, liver).
GN SLC2A2 OR GLUT2 OR GLUT-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=90098776; PubMed=2602116;
RA Suzue K., Lodish H.F., Thorens B.;
RT "Sequence of the mouse liver glucose transporter.";
RL Nucleic Acids Res. 17:10099-10099(1989).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=89366666; PubMed=2771649;
RA Asano T., Shibasaki Y., Lin J.L., Akanuma Y., Takaku F., Oka Y.;
RT "The nucleotide sequence of cDNA for a mouse liver-type glucose
RT transporter protein.";
RL Nucleic Acids Res. 17:6386-6386(1989).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851;
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DR EMBL; AB047629; BAB12153.1; -
DR InterPro; IPR004157; OATP_Cterm.
DR InterPro; IPR004156; OATP_Nterm.
DR Pfam; PF03137; OATP_C; 1.
DR Pfam; PF03132; OATP_N; 1.
DR TIGRFAMs; TIGR00805; oat; 1.
KW Transmembrane; Transport; Ion transport; Glycoprotein.
FT TRANSMEM 79 99 POTENTIAL.
FT TRANSMEM 111 131 POTENTIAL.
FT TRANSMEM 243 263 POTENTIAL.
FT TRANSMEM 283 303 POTENTIAL.
FT TRANSMEM 317 337 POTENTIAL.
FT TRANSMEM 440 460 POTENTIAL.
FT TRANSMEM 481 501 POTENTIAL.
FT TRANSMEM 533 553 POTENTIAL.
FT DOMAIN 142 205 SER-RICH.
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 410 410 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 582 582 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 602 AA; 66738 MW; 1F02F84170F6C31D CRC64;

Query Match 64.7%; Score 33; DB 1; Length 602;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 IQLFCK 9
| | | | |
Db 9 IQLFCK 14

Search completed: October 14, 2003, 14:34:10
Job time : 8.54167 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 14:33:18 ; Search time 29.8125 Seconds
(without alignments)
77.903 Million cell updates/sec

Title: US-09-881-490-191
Perfect score: 51
Sequence: 1 KCLIQLFCK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp Vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|---------------------|
| 1 | 40 | 78.4 | 157 | 10 Q9SPY9 | Q9spy9 pisum sativ |
| 2 | 40 | 78.4 | 895 | 5 Q8SSZ4 | Q8ssz4 dictyosteli |
| 3 | 39 | 76.5 | 319 | 13 Q9YH55 | Q9yh55 gallus gall |
| 4 | 39 | 76.5 | 798 | 11 Q8BUJ2 | Q8bu j2 mus musculu |
| 5 | 39 | 76.5 | 875 | 11 Q8BY36 | Q8by36 mus musculu |
| 6 | 39 | 76.5 | 944 | 3 Q96WT2 | Q96wt2 phoma betae |
| 7 | 38 | 74.5 | 313 | 13 Q9PSJ5 | Q9psj5 ictalurus p |
| 8 | 38 | 74.5 | 554 | 16 Q988N4 | Q988n4 rhizobium l |
| 9 | 38 | 74.5 | 661 | 11 Q61889 | Q61889 mus musculu |
| 10 | 38 | 74.5 | 662 | 11 Q9WV57 | Q9wv57 rattus norv |
| 11 | 38 | 74.5 | 700 | 10 Q9LRV2 | Q9lr v2 arabidopsis |
| 12 | 38 | 74.5 | 752 | 11 Q9JI82 | Q9ji82 mus musculu |
| 13 | 38 | 74.5 | 2754 | 5 Q8I451 | Q8i451 plasmodium |
| 14 | 37 | 72.5 | 163 | 10 Q9SY46 | Q9sy46 arabidopsis |
| 15 | 37 | 72.5 | 217 | 13 P70015 | P70015 xenopus lae |
| 16 | 37 | 72.5 | 217 | 13 P70017 | P70017 xenopus lae |

| | | | | | | |
|----|----|------|------|----|--------|---------------------|
| 17 | 37 | 72.5 | 217 | 13 | P70027 | P70027 xenopus lae |
| 18 | 37 | 72.5 | 548 | 5 | Q8IRA7 | Q8ira7 drosophila |
| 19 | 37 | 72.5 | 1199 | 5 | Q8I397 | Q8i397 plasmodium |
| 20 | 36 | 70.6 | 192 | 11 | Q9D2J1 | Q9d2j1 mus musculu |
| 21 | 36 | 70.6 | 243 | 4 | Q9H4Y5 | Q9h4y5 homo sapien |
| 22 | 36 | 70.6 | 248 | 11 | Q9D2S1 | Q9d2s1 mus musculu |
| 23 | 36 | 70.6 | 248 | 11 | Q8K2Q2 | Q8k2q2 mus musculu |
| 24 | 36 | 70.6 | 248 | 11 | Q8BW12 | Q8bw12 mus musculu |
| 25 | 36 | 70.6 | 311 | 11 | Q8VFB3 | Q8vfb3 mus musculu |
| 26 | 36 | 70.6 | 476 | 5 | Q8T3V4 | Q8t3v4 drosophila |
| 27 | 36 | 70.6 | 476 | 5 | Q9V309 | Q9v309 drosophila |
| 28 | 36 | 70.6 | 516 | 10 | Q8L6I5 | Q8l6i5 oryza sativ |
| 29 | 36 | 70.6 | 730 | 10 | Q9FMF6 | Q9fmf6 arabidopsis |
| 30 | 36 | 70.6 | 2134 | 12 | Q9YLS4 | Q9yls4 avian encep |
| 31 | 35 | 68.6 | 55 | 6 | Q9GMM7 | Q9gmm7 macaca fasc |
| 32 | 35 | 68.6 | 196 | 12 | O57013 | O57013 grapevine 1 |
| 33 | 35 | 68.6 | 211 | 4 | Q96PJ7 | Q96pj7 homo sapien |
| 34 | 35 | 68.6 | 217 | 13 | P70016 | P70016 xenopus lae |
| 35 | 35 | 68.6 | 236 | 6 | Q9XS71 | Q9xs71 bos taurus |
| 36 | 35 | 68.6 | 251 | 4 | Q96AR4 | Q96ar4 homo sapien |
| 37 | 35 | 68.6 | 259 | 11 | Q8BHJ0 | Q8bhj0 mus musculu |
| 38 | 35 | 68.6 | 319 | 2 | Q9RMD1 | Q9rmd1 acinetobact |
| 39 | 35 | 68.6 | 341 | 5 | O18100 | O18100 caenorhabdi |
| 40 | 35 | 68.6 | 432 | 16 | Q8ZR79 | Q8zr79 salmonella |
| 41 | 35 | 68.6 | 432 | 16 | Q8Z8Q7 | Q8z8q7 salmonella |
| 42 | 35 | 68.6 | 462 | 10 | Q9CA73 | Q9ca73 arabidopsis |
| 43 | 35 | 68.6 | 584 | 16 | Q9ZCD7 | Q9zcd7 rickettsia |
| 44 | 35 | 68.6 | 604 | 10 | Q8RZK3 | Q8rz k3 oryza sativ |
| 45 | 35 | 68.6 | 614 | 10 | Q9FJY0 | Q9fjy0 arabidopsis |

ALIGNMENTS

RESULT 1

| | | | | | |
|--------|---|---|----------------|------------------|---------|
| Q9SPY9 | ID | Q9SPY9 | PRELIMINARY; | PRT; | 157 AA. |
| AC | Q9SPY9; | | | | |
| DT | 01-MAY-2000 | (TREMBLrel. 13, Created) | | | |
| DT | 01-MAY-2000 | (TREMBLrel. 13, Last sequence update) | | | |
| DT | 01-MAR-2003 | (TREMBLrel. 23, Last annotation update) | | | |
| DE | Putative NBS-LRR type disease resistance protein (Fragment). | | | | |
| GN | RGA-G3A. | | | | |
| OS | Pisum sativum (Garden pea). | | | | |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | | | |
| OC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; | | | | |
| OC | eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum. | | | | |
| OX | NCBI_TaxID=3888; | | | | |
| RM | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=cv. B880-221; | | | | |
| RA | Timmerman-Vaughan G., Frew T., Weeden N.F.; | | | | |
| RT | *Characterization and linkage mapping of R-gene analogous DNA | | | | |
| RT | sequences in pea (Pisum sativum L.)."; | | | | |
| RL | Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases. | | | | |
| DR | EMBL; | AF123703; | AAD52719.1; | -; | |
| DR | InterPro; | IPR002114; | HPR_Serp_site. | | |
| DR | InterPro; | IPR002182; | NB-ARC. | | |
| DR | Pfam; | PF00931; | NB-ARC; | 1. | |
| DR | PROSITE; | PS00589; | PTS_HPR_SER; | 1. | |
| FT | NON_TER | 1 | | | |
| FT | NON_TER | 157 | 157 | | |
| SQ | SEQUENCE | 157 AA; | 17949 MW; | 9FA495ECC7ABD946 | CRC64; |

Query Match 78.4%; Score 40; DB 10; Length 157;

Best Local Similarity 66.7%; Pred. No. 2.2;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCLIQLFCK 9

||:||||:

Db 125 KCALQLFCQ 133

RESULT 2
Q8SSZ4 PRELIMINARY; PRT; 895 AA.
ID Q8SSZ4
AC Q8SSZ4;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann K., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and Analysis of Chromosome 2 of Dictyostelium.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC116330; AAL96724.1; -.
DR InterPro; IPR006768; CwfJ_C_1.
DR InterPro; IPR006767; CwfJ_C_2.
DR Pfam; PF04677; CwfJ_N_1; 1.
DR Pfam; PF04676; CwfJ_N_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 895 AA; 104485 MW; 94895D6A284E3384 CRC64;

Query Match 78.4%; Score 40; DB 5; Length 895;
Best Local Similarity 77.8%; Pred. No. 8.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCLIQFCK 9
DB 739 KCLIQMPAK 747

RESULT 3
Q9YH55 PRELIMINARY; PRT; 319 AA.
ID Q9YH55
AC Q9YH55;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Olfactory receptor-like protein COR3'beta.
GN COR3'BETA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94140361; PubMed-8307571;
RA Reitman M., Grasso J.A., Blumenthal R., Lewit P.;
RT "Primary sequence, evolution, and repetitive elements of the Gallus
gallus (chicken) beta-globin cluster.";
RL Genomics 18:616-626(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Saitoh N., Pikaart M.J., Recillas-Targa F., Felsenfeld G.;
RT "The 3' chromatin boundary of the chicken beta globin locus.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; L17432; AAD03349.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 319 AA; 35651 MW; 73818123E9F25D06 CRC64;

Query Match 76.5%; Score 39; DB 13; Length 319;
Best Local Similarity 85.7%; Pred. No. 6.1;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 CLIQLFC 8
DB 97 CLIQMFC 103
RESULT 4
Q8BUJ2 PRELIMINARY; PRT; 798 AA.
ID Q8BUJ2
AC Q8BUJ2;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE VPS39/VAM6-like protein homolog (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE-22354683; PubMed-12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK084743; BAC39271.1; -.
FT NON_TER 798 798
SQ SEQUENCE 798 AA; 91720 MW; 6D11A25DF46B358B CRC64;

Query Match 76.5%; Score 39; DB 11; Length 798;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 CLIQLFCK 9
DB 610 CLIQLYCE 617

RESULT 5
Q8BY36 PRELIMINARY; PRT; 875 AA.
ID Q8BY36
AC Q8BY36;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE VPS39/VAM6-like protein homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE-22354683; PubMed-12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK042253; BAC31205.1; -.
SQ SEQUENCE 875 AA; 100724 MW; 9BA3B0061BBF38F6 CRC64;

Query Match 76.5%; Score 39; DB 11; Length 875;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 CLIQLFCK 9
DB 610 CLIQLYCE 617

```
RESULT 6
Q96WT2
ID Q96WT2 PRELIMINARY: PRT: 944 AA.
AC Q96WT2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Aphidicolan-16beta-ol synthase.
GN ACS.
OS Phoma betae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC Dothideomycetes et Chaetothyriomycetes incertae sedis; Phoma.
OX NCBI_TaxID=137527;
RN [1]
RP SEQUENCE FROM N.A.
RA Oikawa H., Toyomasu T., Toshima H., Ohashi S., Kawaide H., Kamiya Y.,
RA Otsuka M., Shinoda S., Mitsuhashi W., Sassa T.;
RT "Cloning and functional expression of cDNA encoding aphidicolan-
RT 16beta-ol synthase: A key enzyme responsible for formation of an
RT unusual diterpene skeleton in biosynthesis of aphidicolin.";
RL J. Am. Chem. Soc. 2001;5154-5155(2001).
DR EMBL: AB049075; BAB62102.1; -.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene_synth; 1.
SQ SEQUENCE 944 AA; 106580 MW; 41C781506F236CE5 CRC64;

Query Match 76.5%; Score 39; DB 3; Length 944;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CLIQLFCK 9
Db 911 CLIDMFCK 918

RESULT 7
Q9PSJ5
ID Q9PSJ5 PRELIMINARY: PRT: 313 AA.
AC Q9PSJ5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Odorant receptor 8 (olfactory receptor 8).
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93201590; PubMed=7916654;
RA Ngai J., Dowling M.M., Buck L., Axel R., Chess A.;
RT "The family of genes encoding odorant receptors in the channel
RT catfish.";
RL Cell 72:657-666(1993).
DR EMBL: L09222; AAK14716.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 313 AA; 35552 MW; 0DA8FA06F6F700963 CRC64;

Query Match 74.5%; Score 38; DB 13; Length 313;
Best Local Similarity 71.4%; Pred. No. 9.5;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 CLIQLFCK 8
Db 98 CLVQMEC 104
```

```
RESULT 8
Q988N4
ID Q988N4 PRELIMINARY: PRT: 554 AA.
AC Q988N4;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein mll6665.
GN MLL6665.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE-21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003009; BAB52913.1; -.
DR InterPro; IPR001466; Beta_lactamase.
DR Pfam; PF00144; beta-lactamase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 554 AA; 59616 MW; 8453E0738C56F67F CRC64;

Query Match 74.5%; Score 38; DB 16; Length 554;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 8
Db 495 KCLIEYFC 502

RESULT 9
Q61889
ID Q61889 PRELIMINARY: PRT: 661 AA.
AC Q61889;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MPS1 protein precursor (Fragment).
GN MPEGL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR;
RX MEDLINE-95195232; PubMed=7888681;
RA Spillsbury K., O'Mara M.A., Wu W.M., Rowe P.B., Symonds G.,
RA Takayama Y.;
RT "Isolation of a novel macrophage-specific gene by differential cDNA
RT analysis.";
RL Blood 85:1620-1629(1995).
DR EMBL; L20315; AAA73957.1; -.
DR MGD; MGI:1333743; Mpeg1.
DR InterPro; IPR001862; MAC_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00457; MACPF; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 26 POTENTIAL.
SQ SEQUENCE 661 AA; 73166 MW; 95D2B55E0DB0C814 CRC64;

Query Match 74.5%; Score 38; DB 11; Length 661;
```

```
Best Local Similarity 55.6%; Pred. No. 17;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 9
Db 434 KCILKIFCK 442

RESULT 10
Q9WV57
ID Q9WV57 PRELIMINARY; PRT; 662 AA.
AC Q9WV57;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Mpg-1 protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Chen S., Garcia G.F., Xia Y., Wilson C.R., Ku G., Feng L.;
RT "Immunoneutralization of the Macrophage Gene-1 Product Attenuates
Renal Injury in Experimental Glomerulonephritis in WKY rats.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF156540; AAD38417.1; -.
DR InterPro; IPR001862; MACPF; 1.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00457; MACPF; 1.
DR SEQUENCE 662 AA; 73327 MW; 98BC5F14B27BFC61 CRC64;

Query Match 74.5%; Score 38; DB 11; Length 562;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 9
Db 435 KCTLKIFCK 443

RESULT 11
Q9LRV2
ID Q9LRV2 PRELIMINARY; PRT; 700 AA.
AC Q9LRV2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Selenium-binding protein-like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
features of the regions of 4,504,864 bp covered by sixty P1 and TAC
clones.";
RL DNA Res. 7:131-135(2000).
DR EMBL; AB028611; BAB01836.1; -.
DR InterPro; IPR002885; PPR.
DR Pfam; PF01535; PPR; 12.
DR TIGRFAMs; TIGR00756; PPR; 8.
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SQ SEQUENCE 700 AA; 79194 MW; 1525A5DE7F242682 CRC64;

Query Match 74.5%; Score 38; DB 10; Length 700;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 CLIQLFCK 9
Db 638 CMIELYCK 645

RESULT 12
Q9JI82
ID Q9JI82 PRELIMINARY; PRT; 752 AA.
AC Q9JI82;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE FPCS50.
GN PFPL OR EPCS50.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hemberger M.C., Himmelbauer H., Ruschmann J., Zeitz C., Fundele R.H.;
RT "cDNA subtraction cloning reveals novel genes whose temporal and
spatial expression indicates association with trophoblast invasion.";
RL Dev. Biol. 0:0-0(2000).
DR EMBL; AF250839; AAF81276.1; -.
DR MGD; MGI:1860266; Pfpl.
DR InterPro; IPR001862; MAC_perforin.
DR SMART; SM00457; MACPF; 1.
DR SEQUENCE 752 AA; 83921 MW; C2B8ED4D871D894F CRC64;

Query Match 74.5%; Score 38; DB 11; Length 752;
Best Local Similarity 44.4%; Pred. No. 19;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 9
Db 438 KCILKIFCR 446

RESULT 13
Q8I451
ID Q8I451 PRELIMINARY; PRT; 2754 AA.
AC Q8I451;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN PFE0250W.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,
RA Hall N., Bowman S., Churcher C., Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255708; PubMed=12368867;
RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden P., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
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RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch F.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrell B.G;
RT *Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.*;
RL Nature 419:527-531(2002).
DR EMBL; AL929351; CAD51416.1; -.
KW Hypothetical protein.
SQ SEQUENCE 2754 AA; 328673 MW; 44FB731EF95DE073 CRC64;

Query Match 74.5%; Score 38; DB 5; Length 2754;
Best Local Similarity 55.6%; Pred. No. 53;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCLIQLFCK 9
Db 2022 KCMYTMFCK 2030
|||: |||

RESULT 14
Q9SY46 PRELIMINARY; PRT; 163 AA.
AC Q9SY46;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical 18.6 kDa protein.
GN T5L23.18 OR A14G03680.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Zhong J., Ma P., Parnell L.D., Chen C.-N., Chen E.Y.;
RT *BAC T5L23 from chromosome IV, position 19 cM.*;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Zhong J., Ma P., Parnell L.D., Chen C.N., Chen E.Y., Mewes H.W.,
RA Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005142; AAD15324.1; -.
DR EMBL; AL161497; CAB77853.1; -.
KW Hypothetical protein.
SQ SEQUENCE 163 AA; 18568 MW; 658F2CE68C39EF4F CRC64;

Query Match 72.5%; Score 37; DB 10; Length 163;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCLIQLF 7
Db 7 KCLIQLF 13
|||||

RESULT 15
P70015 PRELIMINARY; PRT; 217 AA.
ID P70015
AC P70015;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Olfactory receptor (Fragment).
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OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Freitag J.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96112032; PubMed=8845161;
RA Freitag J., Krieger J., Strotman J., Breer H.;
RT *Two classes of olfactory receptors in Xenopus laevis.*;
RL Neuron 15:1383-1392(1995).
DR EMBL; Y08346; CAA69632.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 217
SQ SEQUENCE 217 AA; 24780 MW; 2590F8AE177CDFE2 CRC64;

Query Match 72.5%; Score 37; DB 13; Length 217;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CLIQLFC 8
Db 27 CLFQLFC 33
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Search completed: October 14, 2003, 14:37:00
Job time : 31.8125 secs
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PALM Pay Periods for FY03

| PP | Beginning Date | Ending Date | |
|------|--------------------|--------------------|--------------------------|
| 0301 | October 01, 2002 | October 19, 2002 | |
| 0302 | October 20, 2002 | November 02, 2002 | |
| 0303 | November 03, 2002 | November 16, 2002 | |
| 0304 | November 17, 2002 | November 30, 2002 | |
| 0305 | December 01, 2002 | December 14, 2002 | End of 1st Quarter |
| 0306 | December 15, 2002 | December 28, 2002 | |
| 0307 | December 29, 2002 | January 11, 2003 | |
| 0308 | January 12, 2003 | January 25, 2003 | |
| 0309 | January 26, 2003 | February 08, 2003 | |
| 0310 | February 9, 2003 | February 22, 2003 | |
| 0311 | February 23, 2003 | March 08, 2003 | |
| 0312 | March 9, 2003 | March 22, 2003 | End of 2nd Quarter |
| 0313 | March 23, 2003 | April 05, 2003 | |
| 0314 | April 06, 2003 | April 19, 2003 | |
| 0315 | April 20, 2003 | May 03, 2003 | |
| 0316 | May 04, 2003 | May 17, 2003 | |
| 0317 | May 18, 2003 | May 31, 2003 | |
| 0318 | June 01, 2003 | June 14, 2003 | |
| 0319 | June 15, 2003 | June 28, 2003 | End of 3rd Quarter |
| 0320 | June 29, 2003 | July 12, 2003 | |
| 0321 | July 13, 2003 | July 26, 2003 | |
| 0322 | July 27, 2003 | August 9, 2003 | |
| 0323 | August 10, 2003 | August 23, 2003 | |
| 0324 | August 24, 2003 | September 06, 2003 | |
| 0325 | September 07, 2003 | September 20, 2003 | |
| 0326 | September 21, 2003 | September 30, 2003 | End of 4th Quarter |